

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2002, 02:08:58 ; Search time 51 Seconds
(without alignments)
3589.922 Million cell updates/sec

Title: US-09-575-580B-2
Perfect score: 597
Sequence: 1 atggaggagggtgactgca.....caccgatccaccttagctga 597

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	398	66.7	2174	2 US-08-665-040-1	Sequence 1, Appli
2	38.4	6.4	3303	1 US-08-081-610-3	Sequence 3, Appli
3	37.8	6.3	7218	1 US-08-232-463-14	Sequence 14, Appl
4	37.6	6.3	7130	4 US-09-056-105-31	Sequence 31, Appl
5	37.2	6.2	50937	4 US-09-428-517-1	Sequence 1, Appli
6	36.2	6.1	6328	4 US-08-913-832A-1	Sequence 1, Appli
7	36.2	6.1	6328	4 US-09-249-181A-1	Sequence 1, Appli
8	36	6.0	911	2 US-08-924-759-9	Sequence 9, Appli
9	36	6.0	911	3 US-09-248-335-9	Sequence 9, Appli
10	34	5.7	1296	1 US-07-816-283-9	Sequence 9, Appli
11	34	5.7	1296	1 US-08-417-103-9	Sequence 9, Appli
12	34	5.7	2118	4 US-09-221-017B-789	Sequence 789, App
13	33.2	5.6	2277	1 US-08-676-967-2	Sequence 2, Appli
14	33.2	5.6	2277	1 US-08-676-974-2	Sequence 2, Appli
15	33.2	5.6	2277	2 US-09-098-487-2	Sequence 2, Appli
16	33.2	5.6	2289	4 US-09-312-038-3	Sequence 3, Appli
17	33	5.5	2089	1 US-08-552-142A-1	Sequence 1, Appli
18	33	5.5	2089	4 US-09-910-973-1	Sequence 1, Appli
19	33	5.5	2089	4 US-09-499-227-1	Sequence 1, Appli
20	33	5.5	2089	5 PCT-US95-05741-1	Sequence 1, Appli
21	33	5.5	4221	4 US-09-651-656-22	Sequence 22, Appl
22	33	5.5	4221	4 US-09-650-855-22	Sequence 22, Appl
23	32.4	5.4	602	4 US-09-470-191-81	Sequence 81, Appl
24	32.4	5.4	21338	4 US-08-961-527-20	Sequence 20, Appl
25	32.2	5.4	435	4 US-09-397-787-282	Sequence 282, App
26	32	5.4	16442	3 US-08-781-891-208	Sequence 208, App
27	31.8	5.3	3489	2 US-08-728-323A-1	Sequence 1, Appli

28	31.8	5.3	3489	4 US-09-298-568-1	Sequence 1, Appli
29	31.8	5.3	32207	2 US-08-770-379-20	Sequence 20, Appl
30	31.8	5.3	32207	4 US-08-757-669A-20	Sequence 20, Appl
31	31.8	5.3	32207	4 US-09-230-371A-20	Sequence 20, Appl
32	31.6	5.3	7015	4 US-09-177-249-6	Sequence 6, Appli
33	31.6	5.3	36519	3 US-08-923-137-2	Sequence 3, Appli
34	31.2	5.2	16389	4 US-09-741-154-3	Sequence 16, Appl
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37	31	5.2	1930	2 US-08-737-716-11	Sequence 11, Appl
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41	30.8	5.2	1155	4 US-08-818-111-12	Sequence 12, Appl
42	30.8	5.2	1155	4 US-08-818-111-12	Sequence 12, Appl
43	30.8	5.2	1155	4 US-09-056-556-12	Sequence 12, Appl
44	30.8	5.2	1155	4 US-09-072-596-12	Sequence 12, Appl
45	30.8	5.2	28720	4 US-09-341-587-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-08-665-040-1
; Sequence 1, Application US/08665040
; Patent No. 5869318
; GENERAL INFORMATION:
; APPLICANT: ESTIVILL PALLEJA, XAVIER
; APPLICANT: FUENTES, JUAN JOSE
; APPLICANT: PRITCHARD, MELANIE
; TITLE OF INVENTION: A NEW GENE SEQUENCE OF THE
; TITLE OF INVENTION: DOWN SYNDROM CRITICAL REGION OF HUMAN CHROMOSOME 21,
; TITLE OF INVENTION: IDENTIFIED BY A NEW "ALU-SPLICING PCR" TECHNIQUE,
; TITLE OF INVENTION: CODING FOR A PROLINE-RICH PROTEIN (DSCRI) HIGHLY
; TITLE OF INVENTION: EXPRESSED IN FOETEL BRAIN AND IN HEART AND METHOD
; TITLE OF INVENTION: FOR CHARACTERIZING IT.
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LADAS & PARRY
; STREET: 26 WEST 61ST STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10023

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1 FOR DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,040
FILING DATE: JUNE 7, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ES P9501140
FILING DATE: JUNE 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: JANET I. CORD
REGISTRATION NUMBER: 33,778
REFERENCE/DOCKET NUMBER: U010815-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
TELEFAX: (212) 246-8959
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2174 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA for mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

us-09-575-580b-2.rni

Fri Nov 15 07:56:45 2002

ORIGINAL SOURCE: human
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: foetal
TISSUE TYPE: Brain
IMMEDIATE SOURCE: gene library of cDNA
LIBRARY: gene library of cDNA from foetal
CLONE: BC-17.8-1 and BC-17.8-2
POSITION IN GENOME:
CHROMOSOME/SEGMENT: chromosome 21/YAC 72H9
MAP POSITION: 21q22.1-q22.2
FEATURE:
NAME/KEY: cDNA for mRNA, BC-17.8
LOCATION: 1..2174
FEATURE:
NAME/KEY: untranslated 5'
LOCATION: 1..48
FEATURE:
NAME/KEY: coding sequence
LOCATION: 49..560
OTHER INFORMATION: Down Syndrome critical
FEATURE:
NAME/KEY: DSCR1
LOCATION: 1..171 PEPTIDES
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OTHER INFORMATION: - deduced protein
OTHER INFORMATION: - proline-rich protein domains
OTHER INFORMATION: - glutamic acid-rich protein domains
OTHER INFORMATION: - leucine/phenylalanine-rich protein domains
FEATURE:
NAME/KEY: untranslated 3'
LOCATION: 564..2174
FEATURE:
NAME/KEY: 2 poly (A)
LOCATION: 1541..1546 AND 2132..2137
US-08-665-040-1
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Best Local Similarity 87.6%; Pred. No. 2.3e-109;
Matches 447; Conservative 0; Mismatches 60; Indels 3; Gaps 1;
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QY 148 AGCTTCAACAGTGTCCGGATAAATTCAGCAACCCCTTATCTGCAGCGGATGCCAGGCTG 207
DB 118 AGCTTCAACAGTGTGAGTAAATTCAGCAACCCCTTATCTGCAGCGGATGCCAGGCTC 177
QY 208 CGGCTGCACAGACCGAGTTCCTGGGAAAGAAATGAAGTTGATTTTGGCTCAGACTTAA 267
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QY 268 CACATAGGAAGTTACACAGCTGGTCCGCCCAATCCCGACAAACAGTTCTCATCTCCCT 327
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QY 328 CGGCTCTCTCTCCGCTGGTGGTGAACAAAGTAGAAGATGCCACCCCGTCAATAATAC 387
DB 298 CGGCTCTCTCTCCGCTGGTGGTGAACAAAGTAGAAGATGCCACCCCGTCAATAATAC 357
QY 388 GATCTTTTATATGCCATCTCCAGCTGGGCGCAGGAGGAAGTATGAACATGCATGCAGCG 447
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QY 448 ACAGACCCCACTCCAGTGTGGTGGTCCACGTGTGTAGAGTACCAAGAGATGAGGAG 507
DB 418 ACTGACACCACTCCAGCTGGTGGTGGTCCCATGTATGTGAGAGTATCAAGAGAGAGGAA 477
QY 508 GAAGAGGAAGATGAGAGAGATGACAGACCAAGCCCAAAATCATCCAGACAGGAGA 567
DB 478 GAAGAGGAA---ATGGAAGAAATGAGAGAGACCTTAAGCCCAAAATTTATCCAGACAGGAGG 534

QY 568 CCGGAGTACACGCGATCCACCTTAGCTGA 597
DB 535 CCGGAGTACACGCGGATCCACCTTAGCTGA 564
RESULT 2
US-08-081-610-3
Sequence 3, Application US/08081610
Patent No. 5445941
GENERAL INFORMATION:
APPLICANT: Yang, Na N
TITLE OF INVENTION: Materials and Methods for Screening
Anti-Osteoporosis or Serum Lipid Lowering Agents
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti and Witcoff, Ltd.
STREET: 10 S. Wacker Dr.
CITY: Chicago
STATE: IL
COUNTRY: U.S.A
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/081,610
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heahy, Barbara A
REGISTRATION NUMBER: 34,619
REFERENCE/DOCKET NUMBER: 93,402
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3303 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: mRNA
LOCATION: 2170..3303
FEATURE:
NAME/KEY: mRNA
LOCATION: 2214..3303
FEATURE:
NAME/KEY: mRNA
LOCATION: 2219..3303
FEATURE:
NAME/KEY: misc_rna
LOCATION: 3301..3303
OTHER INFORMATION: /note= "CDS Start, codon start = 1,
OTHER INFORMATION: translation M"
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 2170..2176
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1896..2306
OTHER INFORMATION: /note= "pb-301 -301 to +110"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1976..2306
OTHER INFORMATION: /note= "pb-221 -221 to +110"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2106..2306
OTHER INFORMATION: /note= "pb-91 -91 to +110"

; APPLICANT: Shah, Sanjay Krishnakant
; APPLICANT: McDaniel, Robert

us-09-575-580b-2.rni

Fri Nov 15 07:56:45 2002

```

; APPLICANT: Tang, Li
; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 30062-20029.00
; CURRENT APPLICATION NUMBER: US/09/428,517
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 60/120,254
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/106,100
; EARLIER FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 50937
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant DNA
US-09-428-517-1
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; Query Match
; Best Local Similarity 56.6%; Pred. No. 0.63; Indels 0; Gaps 0;
; Mismatches 69; Conservative 0;
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; 2 TGAGGAGGTGGATCTGCAGGACCTGCGGAGCGCCACCATCGCTGCCACCTGGACCCGC 61
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; QY 62 CGGTGTTCTGGAGCGCTGTCGCGGCGCCAAATTTGAATCCCTCTTCAGACATATGACA 121
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; Db 8827 CGGTGCTCTTCGACCCACCGCCGCGGCGGCACTGGCAGCGTCTCTCCAGGCGCAGCA 8886
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; QY 122 AG 123
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; Db 8887 CG 8888
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; RESULT 6
; US-09-913-832A-1
; Sequence 1, Application US/08913832A
; Patent No. 6329517
; GENERAL INFORMATION:
; APPLICANT: Seelig, Hans Peter
; TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
; FILE REFERENCE: 8484-0030-999
; CURRENT APPLICATION NUMBER: US/08/913,832A
; CURRENT FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: PCT/DE96/00444
; PRIOR FILING DATE: 1996-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6328
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(5736)
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; Query Match
; Best Local Similarity 53.1%; Pred. No. 0.5; Indels 0; Gaps 0;
; Mismatches 77; Conservative 0;
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; QY 421 GGAGAGAGTATGAACCTGCATCGAGGAGAGAGAGAGAGAGATGGAGAGATGAAGAGACCC 540
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; Db 4921 GTAGAGAGGTGGAGGAAAGTCTAGCAATAGATCTGACCCCTATTGTGTAGAGACAAA 4980
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; QY 481 TGTGAGAGTGCACCAAGAGAGATGAGGAGAGAGAGAGAGAGATGGAGAGATGAAGAGACCC 540
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; Db 4981 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040
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; QY 541 AAGCCCAAAATCATCCAGACACGGA 565
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;
; Db 5041 AAGGACCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
;
;
; RESULT 8
; US-08-924-759-9
; Sequence 9, Application US/08924759
; Patent No. 5962229
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,759
; FILING DATE:
; CLASSIFICATION: 435

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; RESULT 7
; US-09-249-181A-1
; Sequence 1, Application US/09249181A
; Patent No. 6440679
; GENERAL INFORMATION:
; APPLICANT: Seelig, Hans Peter
; TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
; FILE REFERENCE: 8484-0059-999
; CURRENT APPLICATION NUMBER: US/09/249,181A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/913,832
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: PCT/DE96/00444
; PRIOR FILING DATE: 1996-03-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6328
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(5736)
;
; Query Match
; Best Local Similarity 53.1%; Pred. No. 0.5; Indels 0; Gaps 0;
; Mismatches 77; Conservative 0;
;
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; Db 4981 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040
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;
; QY 541 AAGCCCAAAATCATCCAGACACGGA 565
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;
; Db 5041 AAGGACCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5065
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;
; RESULT 8
; US-08-924-759-9
; Sequence 9, Application US/08924759
; Patent No. 5962229
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,759
; FILING DATE:
; CLASSIFICATION: 435

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; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/816,283
; FILING DATE: 19911231
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-816-283-9

Query Match 5.7%; Score 34; DB 1; Length 1296;
Best Local Similarity 56.1%; Pred. No. 1.1;
Matches 64; Conservative 0; Mismatches 50; Indels 0; Gaps

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QY 529 ATGAGAGACCAACCCCAAAATCATCCAGACCGGACCGGAGTACACACCG 582
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Ddb 1111 AGGGAGGGGGGCAAGGGGAAGAGATGAACGGCGGGTCAGCCACGATCACGCAG 1164

RESULT 11
US-08-417-103-9
; Sequence 9, Application US/08417103
; Patent No. 5723299
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamada, Yuichiro
; APPLICANT: Seino, Susumu
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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Fri Nov 15 07:56:45 2002

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APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/816,283
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 28..1281
US-08-417-103-9

Query Match
Best Local Similarity 56.1% Pred. No. 1,1:
Matches 64; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 469 GTGGTCCAGCTGTGTGAGAGTGCACACAGAAATCAGGAGGAAGGAAGATGGAGAGA 528
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Db 1051 GTGGGCCCCCGAGAGAACTGAGGAGGAGGATGAGGAGGAGGAGGATGGGAGGAGAGC 1110
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QY 529 ATGAAGAGACCCAGCCCCAAATCATCCAGACACGAGAGACGGGAGTACACCG 582
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Db 1111 AGGAGGGGGGCAAGGGGAGGAGATGAACGCCCGGTACCGAGATCACCCAG 1164
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RESULT 12
 US-09-221-0178-789/C
 ; Sequence 789, Application US/09221017B
 ; Patent No. 644799
 ; GENERAL INFORMATION:
 ; APPLICANT: Ross, Bruce C.
 ; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
 ; NUMBER OF SEQUENCES: 1120
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 PAGE MILL ROAD
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/221.017B
 ; FILING DATE: 23-DEC-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA: Pp1182
 ; APPLICATION NUMBER: 31-DEC-1997
 ; FILING DATE: 31-DEC-1997
 ; PRIOR APPLICATION DATA: Pp1546
 ; APPLICATION NUMBER: 30-JAN-1998
 ; FILING DATE: 30-JAN-1998
 ; PRIOR APPLICATION DATA: Pp2911
 ; APPLICATION NUMBER: 09-APR-1998
 ; FILING DATE: 09-APR-1998
 ; PRIOR APPLICATION DATA: PCT/AU98/01023
 ; APPLICATION NUMBER: 10-DEC-1998
 ; FILING DATE: 10-DEC-1998

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ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELEPHONE: 650-813-5600
TELEPHONE: 650-494-0792
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 789:
SEQUENCE CHARACTERISTICS:
LENGTH: 2118 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...2118
US-09-221-017B-789

Query Match          5.7%; Score 34; DB 4; Length 2118;
Best Local Similarity 57.5%; Pred. No. 1.4;
Matches 61; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY   147 GAGGCTTCAAAACGGTCGCCGAATAACTCAGACAACCCGTATCTCGACCCGATCCCAGGCT 206
Db   1380 GAGTGCTCTATGTCGAGGAANAATCCGCTCCGCACGATATGTAGACAATACAGGGGT 1321
QY   207 GCGGCTGCACAGAACCAGTTCCTGGGGAAGGAATGAAGTTGAT 252
Db   1320 TCGTCGGCAAGTGACGGAATCCCTGCCGAGAAAATCAACTTTTT 1275

RESULT 13
US-08-676-967-2
; Sequence 2, Application US/08676967
; Patent No. 5747317
; GENERAL INFORMATION:
; APPLICANT: COLLINS, KATHLEEN
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,967
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCH96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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Search completed: November 15, 2002, 03:30:28
Job time : 83 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2002, 00:52:13 ; Search time 2653 Seconds
(without alignments)
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Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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35: em_htg_rod.*
36: em_htg_mam.*
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39: em_hngo_hum.*
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41: em_hngo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	592.2	99.2	621	10	AF282255	Mus muscu
4	592.2	99.2	2125	10	AF260717	Mus muscu
5	515.8	86.4	597	6	AX365315	Sequence
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7	511	85.6	2141	10	AF263239	Mus muscu
8	511	85.6	2198	10	BC013551	Mus muscu
9	507.2	85.0	2224	10	AF263240	Mus muscu
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12	481.8	80.7	2289	9	BC002864	Homo sapi
13	481.8	80.7	2407	9	AK092184	Homo sapi
14	430.8	72.2	626	10	AB075973	Rattus no
15	427.8	71.7	2216	10	CG060263	Cricetus
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26	335	56.1	562	9	HS053821	Homo sapien
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28	211	35.3	3159	6	AX420425	Sequence
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33	193	32.3	3184	6	AX329596	Sequence
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36	193	32.3	3184	6	AX420436	Sequence
37	193	32.3	3184	9	HUMZAK14	mRNA
38	186.4	31.2	720	6	AX365333	Sequence
39	186.4	31.2	720	9	AF176117	Homo sapi
40	186.4	31.2	828	6	AX365330	Sequence
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43	184.6	30.9	615	6	AX420432	Sequence
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ALIGNMENTS

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AX365312
LOCUS
DEFINITION
Accession
VERSION
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1
AUTHORS
TITLE
Williams, S.R. and Rothermel, B.
Methods and compositions relating to muscle selective calceinurin
interacting protein (mcip)
AX365312
Sequence 2 from Patent WO0204491.
AX365312
AX365312.1 GI:18697043
597 bp
DNA
linear
PAT 15-FEB-2002

us-09-575-580b-2.ige

Fri Nov 15 07:56:43 2002

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 597)
AUTHORS Rothermel, B.A., Vega, R.B., Yang, J., Wu, H., Bassel-Duby, R.S. and
Williams, R.S.
TITLE A Protein Encoded within the Down Syndrome Critical Region is
Enriched in Striated Muscles and Inhibits Calcineurin Signaling
J. Biol. Chem. (2000) In press
REFERENCE 2 (bases 1 to 597)
AUTHORS Rothermel, B.A., Vega, R.B., Yang, J., Wu, H., Bassel-Duby, R.S. and
Williams, R.S.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-2000) Internal Medicine, University of Texas
Southwestern Medical Center, 5323 Harry Hines Boulevard, Dallas, TX
75390, USA
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Best Local Similarity 100.0%; Pred. No. 1.1e-148; Indels 0; Gaps 0;
Matches 597; Conservative 0; Mismatches 0;
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LOCUS Mus musculus myocyte-enriched calcineurin interactin protein 1
DEFINITION splice variant 1 mRNA, complete cds.
ACCESSION AF237789
VERSION AF237789.1 GI:7542525
KEYWORDS Mus musculus.
SOURCE

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RESULT 3
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LOCUS Mus musculus Down syndrome candidate region 1 protein (Dscr1) mRNA,
DEFINITION complete cds.
ACCESSION AF282255
VERSION AF282255.1 GI:9652249
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 621)
Strippoli,P., Petrini,M., Lenzi,L., Carinci,P. and Zannotti,M.
TITLE The murine DSCR1-like (Down syndrome candidate region 1) gene
family: conserved synteny with the human orthologous genes
JOURNAL Gene 257 (2), 223-232 (2000)
MEDLINE 20534792
PUBMED 11080588
REFERENCE 2 (bases 1 to 621)
AUTHORS Strippoli,P., Petrini,M., Lenzi,L., Carinci,P. and Zannotti,M.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Istituto di Istologia ed Embriologia
Generale, Universite di Bologna, Via Belmeloro, 8, Bologna, BO
40126, Italy
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CESQNEDEEEMRMKRPKIQTREPTPIHLS"
BASE COUNT 166 a 179 c 159 g 117 t
ORIGIN

Query Match 99.2%; Score 592.2; DB 10; Length 621;
Best local Similarity 99.5%; Pred. No. 2.2e-147;
Matches 594; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 8 ATGGAGGAGTGGATCGAGGACCTGCGGAGCGCCACCATCGCTGCCACCTGGACCG 67
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QY 61 CGCGTGTTCGTGGAGCGCTGTGCGGGGCCAAATTTGAATCCCTCTTCAGAACATATGAC 120
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Db 68 CGCGTGTTCGTGGAGCGCTGTGCGGGGCCAAATTTGAATCCCTCTTCAGAACATATGAC 127
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QY 121 AAGGACACACCTTCCAGTATTTAAGAGCTTCAACAGTGTCCGGATAAACTTCAGCAAC 180
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Db 128 AAGGACACACCTTCCAGTATTTAAGAGCTTCAACAGTGTCCGGATAAACTTCAGCAAC 187

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QY 241 ATGAAGTGTATTTTGTCTCAGACTTTTACACATAGGAAGTTCACACCTGGCTCCGCCCAAT 300
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Db 248 ATGAAGTGTATTTTGTCTCAGACTTTTACACATAGGAAGTTCACACCTGGCTCCGCCCAAT 307
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QY 301 CCGGACAAACAGTTCCTCATCTCCCTCCGGCTCTCTCCCGTTGGCTGGGAACAAGTA 360
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Db 308 CCGGACAAACAGTTCCTCATCTCCCTCCGGCTCTCTCCCGTTGGCTGGGAACAAGTA 367
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QY 361 GAAGATGCCACCCCGCTCATAAATTACGATCTTTTATATGCCATCTCCCAAGCTGGGGCCA 420
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QY 421 GGAGAGAATATGAACATGTCATGTCAGCGAGAGAGAGAGAGATGGAGAGATGAAGAGACCC 540
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RESULT 4
AF260717 2125 bp mRNA linear ROD 22-MAR-2001
LOCUS Mus musculus Down syndrome candidate region 1 (Dscr1) mRNA, complete
DEFINITION cds.
ACCESSION AF260717
VERSION AF260717.1 GI:7839596
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2125)
Casas,C., Martinez,S., Pritchard,M.A., Fuentes,J.J., Nadal,M.,
Guimera,J., Arbones,M., Florez,J., Soriano,E., Estivill,X. and
Alcantara,S.
TITLE Dscr1, a novel endogenous inhibitor of calcineurin signaling, is
expressed in the primitive ventricle of the heart and during
neurogenesis
JOURNAL Mech. Dev. 101 (1-2), 289-292 (2001)
MEDLINE 21152920
PUBMED 11231093
REFERENCE 2 (bases 1 to 2125)
AUTHORS Fuentes,J.J., Pritchard,M., Pucharcas,C. and Estivill,X.
TITLE Down syndrome candidate region 1 (Dscr1), one of three
alternatively spliced exon 1
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2125)
AUTHORS Fuentes,J.J., Pritchard,M., Pucharcas,C. and Estivill,X.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2000) Centre de Genetica Medica i Molecular, IRO,
Avia, Castelldefels Km. 2,7, L'Hospitalet de Llobregat, Barcelona
08907, Spain
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us-09-575-580b-2.rge

Fri Nov 15 07:56:43 2002

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Matches 535;		Conservative				Length 597;	
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QY		271		ATAGGAAGTTTCAACCTGGCTCCGCCCAATCCGACAAACAGTTCTCTATCTCCCTCCG		330	
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Db		391		CTTTTATATGCCATCTCCAGCTGGCGCCAGGAGAGAGTGAAGTCACTGCATGCAGCGACA		450	
QY		451		GACCCCACTCCAGTGTGTGTCAGCTGTGTGAGAGTGAAGTCACTGCATGCAGCGAGAA		510	
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LOCUS		AF237790		Mus musculus myocyte-enriched calineurin interactin protein 1		linear	
DEFINITION		splice variant 4 mRNA, complete cds.					
ACCESSION		AF237790.1		GI:7542528			
VERSION		AF237790.1					
KEYWORDS		Mus musculus.					
SOURCE		Mus musculus					
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					

REFERENCE 1 (bases 1 to 597)
AUTHORS Rothermel,B.A., Vega,R.B., Yang,J., Wu,H., Bassel-Duby,R.S. and Williams,R.S.
TITLE A Protein Encoded within the Down Syndrome Critical Region is Enriched in Striated Muscles and Inhibits Calcineurin Signaling
JOURNAL J. Biol. Chem. (2000) in press
REFERENCE 2 (bases 1 to 597)
AUTHORS Rothermel,B.A., Vega,R.B., Yang,J., Wu,H., Bassel-Duby,R.S. and Williams,R.S.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-2000) Internal Medicine, University of Texas Southwestern Medical Center, 5323 Harry Hines Boulevard, Dallas, TX 75390, USA

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DEFINITION alternatively spliced.
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VERSION AF263239.1 GI:8102011
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SOURCE Mus musculus.
ORGANISM Mus musculus.
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REFERENCE 1 (bases 1 to 2141)
AUTHORS Fuentes,J.J., Pritchard,M.A., Pucharcos,C. and Estivill,X.
TITLE Down syndrome candidate region 1 (Dscr1), one of three alternatively spliced exon 1 transcripts
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2141)
AUTHORS Fuentes,J.J., Pritchard,M.A., Pucharcos,C. and Estivill,X.
TITLE Direct Submission
JOURNAL Submitted (02-MAY-2000) Centre de Genetica Medica i Molecular, IRO, Avia, Castelldefels Km. 2.7, L'Hospitalet de Llobregat, Barcelona 08907, Spain
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DEFINITION clone MGC:19348 IMAGE:4236038, mRNA, complete cds.
ACCESSION BC013551
VERSION BC013551.1 GI:15488840
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2198)
Strausberg, R.
Direct Submission
Submitted (04-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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LOCUS Mus musculus calcineurin inhibitor mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF263240
VERSION AF263240.1 GI:8102013
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 2224)
Fuentes, J.J., Pritchard, M.A., Pucharcos, C. and Estivill, X.
Down syndrome candidate region 1 (Dscr1), one of three
alternatively spliced exon 1 transcripts
Unpublished
JOURNAL
2 (bases 1 to 2224)
Fuentes, J.J., Pritchard, M.A., Pucharcos, C. and Estivill, X.
Direct Submission
TITLE
JOURNAL
Submitted (02-MAY-2000) Centre de Genetica Medica i Molecular, IRO,
Avia. Castelldefels Km. 2.7, L'Hospitalet de Llobregat, Barcelona
08907, Spain
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ACCESSION    AX365324
VERSION      AX365324.1  GI:18697051
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ORGANISM      Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Williams, S.R. and Rothermel, B.
TITLE        Methods and compositions relating to muscle selective calcineurin
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interacting protein (mclp)
Patent: WO 0204491-A 14 17-JAN-2002;
Board of Regents, The University of Texas System (US) ; Williams,
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ACCESSION    U85266
VERSION      U85266.2  GI:7596913
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 REFERENCE 1 (bases 1 to 2227)
 AUTHORS Fuentes, J.J., Pritchard, M.A., Planas, A.M., Bosch, A., Ferrer, I. and Estivill, X.
 TITLE A new human gene from the Down syndrome critical region encodes a proline-rich protein highly expressed in fetal brain and heart
 JOURNAL Hum. Mol. Genet. 4 (10), 1935-1944 (1995)
 MEDLINE 96121593
 PUBMED 8595418
 REFERENCE 2 (bases 1 to 2227)
 AUTHORS Fuentes, J.J., Pritchard, M.A. and Estivill, X.
 TITLE Genomic organization, alternative splicing, and expression patterns of the DSCR1 (Down syndrome candidate region 1) gene
 JOURNAL Genomics 44 (3), 358-361 (1997)
 MEDLINE 97468152
 PUBMED 9325060
 REFERENCE 3 (bases 1 to 2227)
 AUTHORS Fuentes, J.J., Pritchard, M. and Estivill, X.
 TITLE Direct Submission
 JOURNAL Submitted (14-JAN-1997) Genetica Molecular, Institut de Recerca Oncologica, Autovia de Castelldefels, km 2.7, Hospitalet, Barcelona 08907, Spain
 REFERENCE 4 (bases 1 to 2227)
 AUTHORS Fuentes, J.J., Pritchard, M. and Estivill, X.
 TITLE Direct Submission
 JOURNAL Submitted (19-APR-2000) Genetica Molecular, Institut de Recerca Oncologica, Autovia de Castelldefels, km 2.7, Hospitalet, Barcelona 08907, Spain
 REMARK Sequence update by submitter
 COMMENT On Apr 19, 2000 this sequence version replaced gi:2612865.
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2289)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NTH-MGC Project URL: http://mgc.nci.nih.gov
 COMMENT Contact: MGC help desk
 Email: cgabps-r@mail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Ruben Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 nisc.mc@nihri.nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspl, R., Lim, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tlonsong, E.E., Touchman, J.W., Taurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Series: IRAL Plate: 15 Row: a Column: 23
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7596913.
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Best Local Similarity 89.1%; Pred. No. 7.9e-118;
Matches 532; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
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DEFINITION
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to DOWN SYNDROME CRITICAL REGION PROTEIN 1.
ACCESSION
AK092184
VERSION
AK092184.1 GI:21750714
KEYWORDS
oligo capping; fls (full insert sequence).

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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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after the differentiation of NT2 neuronal precursor
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Query Match 80.7%; Score 481.8; DB 9; Length 2407;
Best Local Similarity 89.1%; Pred. No. 7.9e-118;
Matches 532; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
QY 1 ATGGAGAGGTGGATCTGCAGGACCTGCGGAGCGCCACCATCCCTGCGACCTGGACCCG 60
Db 218 ATGGAGAGGTGGATCTGCAGGACCTGCGGAGCGCCACCATCCCTGCTCAGCTGGACCCG 277
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuwa,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
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Kikuchi,H., Sugiyama,A., Kawakami,B., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,K., Masuho,Y., Nagai,K. and Isogai,T.
Nagahara,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
Unpublished

2 (bases 1 to 2407)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'-6' 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
Location/Qualifiers

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after the differentiation of NT2 neuronal precursor
cells."

BASE COUNT 607 a 519 c 627 g 654 t
ORIGIN

Query Match 80.7%; Score 481.8; DB 9; Length 2407;
Best Local Similarity 89.1%; Pred. No. 7.9e-118;
Matches 532; Conservative 0; Mismatches 62; Indels 3; Gaps 1;
QY 1 ATGGAGAGGTGGATCTGCAGGACCTGCGGAGCGCCACCATCCCTGCGACCTGGACCCG 60
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Job time : 2658 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2002, 00:51:33 ; Search time 135 Seconds
(without alignments)
9958.837 Million cell updates/sec

Title: US-09-575-580B-2

Perfect score: 597

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	597	100.0	597	24	Human MCIP associa
2	515.8	86.4	597	24	Mouse MCIP associa
3	481.8	80.7	2212	24	Human MCIP associa
4	469	78.6	2358	21	Lung cancer associ
5	426.2	71.4	599	24	Human MCIP associa
6	403.8	67.6	2331	24	Human MCIP associa
7	399.6	66.9	2173	24	Gene #3341 used to
8	398	66.7	2174	20	Human DSCR1 coding
9	392.8	65.8	2348	24	Human DNA sequence

10	211	35.3	934	22	AAF25338	Nucleotide sequenc
11	211	35.3	3159	24	ABA91457	Human Down syndrom
12	207	34.7	442	21	AAC01774	Human secreted pro
13	193	32.3	3184	24	AAD30157	Human MCIP associa
14	193	32.3	3184	24	ABL61768	Colon adenocarcino
15	193	32.3	3184	24	ABL65187	Lung cancer relate
16	186.4	31.2	720	24	AAD30159	Human MCIP associa
17	186.4	31.2	828	24	AAD30158	Human MCIP associa
18	184.6	30.9	615	24	ABA91463	Rat Down syndrome
19	183	30.7	594	24	AAD30154	Mouse MCIP associa
20	144.6	24.2	412	22	ABA56172	Human foetal liver
21	144.6	24.2	412	22	AK04364	Human brain expres
22	144.6	24.2	412	22	AAI14449	Probe #4382 for ge
23	144.6	24.2	412	22	AAI35821	Probe #4507 used t
24	144.6	24.2	412	22	AAI04272	Probe #4263 used t
25	144.6	24.2	412	24	ABS04419	Human genome-deriv
26	144.6	24.2	446	22	ABA43406	Human breast cell
27	144.6	24.2	446	22	ABA53852	Human foetal liver
28	144.6	24.2	446	22	ABA23398	Probe #2084 for ge
29	144.6	24.2	446	22	AAK02113	Human brain expres
30	144.6	24.2	446	22	AAK27563	Human bone marrow
31	144.6	24.2	446	22	AAI12148	Probe #2081 for ge
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33	144.6	24.2	446	22	AAI02061	Probe #2052 used t
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36	123	20.6	486	22	ABA42132	Human breast cell
37	123	20.6	486	22	ABA52554	Human foetal liver
38	123	20.6	486	22	ABA22343	Probe #809 for gen
39	123	20.6	486	22	AAK00816	Human brain expres
40	123	20.6	486	22	AAK26270	Human bone marrow
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ALIGNMENTS

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DT 17-MAY-2002 (first entry)
DE Human MCIP associated DNA #2.
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KW heart failure; cardiomyopathy; heart disease; human; gene; ds.
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OS Homo sapiens.
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FH Key
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XX Williams SR, Rothermel B;
XX WPI: 2002-179698/23.
DR P-PSDB; AAE18911.
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XX Screening for modulators of muscle calcineurin interacting protein
PT (MCIP) binding, expression or phosphorylation, useful for treating
PT cardiac hypertrophy or heart failure, comprises mixing MCIP,
PT calcineurin and a test compound -
XX
XX
XX Claim 95; Page 147-148; 174pp; English.
XX
XX The invention relates to muscle calcineurin interacting proteins (MCIPs)
CC and nucleic acid molecules encoding such proteins. MCIPs form a physical
CC complex with the catalytic subunit of calcineurin and increased levels
CC of MCIPs correspond to a reduced ability of calcineurin to stimulate
CC transcription of certain target genes. The invention also relates to
CC methods for identifying modulators of MCIP binding, expression or
CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
CC may be used for treating cardiac hypertrophy and heart failure.
CC Antibodies to MCIP can be used in characterising the MCIP content of
CC healthy and diseased tissues and subsequently for determining the
CC presence or absence of cardiomyopathy or as predictor of heart disease.
CC The present sequence is human MCIP associated DNA.
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KW heart failure; cardiomyopathy; heart disease; mouse; gene; ds.
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XX 17-JAN-2002.
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XX 06-JUL-2001; 2001WO-US21662.
XX
XX 07-JUL-2000; 2000US-216601P.
XX 13-FEB-2001; 2001US-0782953.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA (WILL/) WILLIAMS S R.
PA (ROTH/) ROTHERMEL B.
XX
XX Williams SR, Rothermel B;
PI
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XX WPI: 2002-179698/23.
DR P-PSDB; AAE18912.
XX
XX Screening for modulators of muscle calcineurin interacting protein
PT (MCIP) binding, expression or phosphorylation, useful for treating
PT cardiac hypertrophy or heart failure, comprises mixing MCIP,
PT calcineurin and a test compound -
XX
XX
XX Disclosure; Page 150-151; 174pp; English..
XX
XX The invention relates to muscle calcineurin interacting proteins (MCIPs)
CC and nucleic acid molecules encoding such proteins. MCIPs form a physical
CC complex with the catalytic subunit of calcineurin and increased levels
CC of MCIPs correspond to a reduced ability of calcineurin to stimulate
CC transcription of certain target genes. The invention also relates to
CC methods for identifying modulators of MCIP binding, expression or
CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
CC may be used for treating cardiac hypertrophy and heart failure.
CC Antibodies to MCIP can be used in characterising the MCIP content of
CC healthy and diseased tissues and subsequently for determining the
CC presence or absence of cardiomyopathy or as predictor of heart disease.
CC The present sequence is mouse MCIP associated DNA.
CC Note: This sequence has been described as human MCIP3 encoding DNA
CC in the specification, however the sequence seems to be a polynucleotide
CC encoding a MCIP associated protein.
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Best Local Similarity 94.4%; Pred. No. 3.3e-145;
Matches 535; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 31 AGCGGCACCATCGCTGCCACCTGGACCCGCGCTGTTCTGGAGCGGCTGTGCGGGCC 90
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Fri Nov 15 07:56:44 2002

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XX cardioactive; immunomodulatory; muscular active; vulnerary;
XX gastrointestinal; nephrotropic; antiinfective; gynecological;
XX antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
XX proliferative disorder; wound healing; infectious disease; ds.
XX
XX Homo sapiens.
XX
XX WO200055180-A2.
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XX 21-SEP-2000.
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XX 08-MAR-2000; 2000WO-US05918.
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XX 12-MAR-1999; 99US-0124270.
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XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
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XX Lung cancer associated gene sequences, referred to as lung cancer
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XX such as lung cancer -
XX
XX Claim 1; Page 805-806; 1425pp; English.
XX
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
XX associated proteins represented in AAB58106 - AAB58548. Lung cancer
XX associated proteins and polynucleotide sequences, their agonists, and
XX antagonists may have neuroprotective; cytostatic; cardioactive;
XX immunomodulatory; muscular active general; vulnerary; gastrointestinal
XX general; nephrotropic; antiinfective; gynecological; or antibacterial
XX activity. The invention also includes antibodies specific for the
XX protein or polynucleotide sequences. The lung cancer associated
XX polynucleotide sequences may be used for detection of lung cancer,
XX chromosome identification, as chromosome markers, and for numerous other
XX diagnostic or research purposes. The proteins may be used to treat
XX disorders such as neural, immune, muscular, reproductive,
XX gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
XX disorders. The proteins may also be used in the treatment of wounds and
XX infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
XX peptide AAB58549 are used in the course of the invention for the
XX identification and characterisation of the polynucleotide and protein
XX sequences.
XX
XX Sequence 2358 BP; 641 A; 482 C; 584 G; 647 T; 4 other;
XX
XX
XX Query Match 78.6%; Score 469; DB 21; Length 2358;
XX Best Local Similarity 88.6%; Pred. No. 8.2e-131;
XX Matches 529; Conservative 2; Mismatches 62; Indels 4; Gaps 2;
XX
XX 1 ATGGAGGAGGTGGATCTCAGGACCTGCCAGCGCCACCATCGCTGCCACCTGGACCCG 60
XX |||||||||||
XX 114 ATGGAGGAGGTGGATCTCAGGACCTGCCAGCGCCACCATCGCTGCCACCTGGACCCG 173
XX |||||||||||
XX 61 CGCGTGTTCGTGGACGGCTGTGGCGGCCAAATTTGAATCCCTTCAGACATATGAC 120
XX |||||||||||
XX 174 CGCGTGTTCGTGGACGGCTGTGGCGGCCAAATTTGAATCCCTTCAGACATATGAC 233
XX |||||||||||
XX 121 AGGACACACCTCTCCAGTATTTTAAAGAGCTTCAAAAGCTGTCCGATATAACTTCAGCAAC 180
XX |||||||||||
XX 234 AAGGACATACCTCTTCAGTATTTTAAAGAGCTTCAAAAGCTTCAAAAGCTTCAGCAAC 293
XX |||||||||||

```

RESULT 5

AAD30151

ID AAD30151 standard; DNA; 599 BP.

XX

AC AAD30151;

XX

DT 17-MAY-2002 (first entry)

XX

XX Human MCIP associated DNA #1.

DE

XX Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;

XX heart failure; cardiomyopathy; heart disease; human; ds.

XX Homo sapiens.

OS

PN WO200204491-A2.

XX

XX 17-JAN-2002.

XX

XX 06-JUL-2001; 2001WO-US21662.

XX

XX 07-JUL-2000; 2000US-216601P.

XX

XX 13-FEB-2001; 2001US-0782953.

XX

XX (TEXA) UNIV TEXAS SYSTEM.

XX

XX (WILL/) WILLIAMS S R.

XX

XX (ROTH/) ROTHERMEL B.

XX

XX Williams SR, Rothermel B;

XX

XX WPI; 2002-179698/23.

XX

XX Screening for modulators of muscle calcineurin interacting protein

XX (MCIP) binding, expression or phosphorylation, useful for treating

XX cardiac hypertrophy or heart failure, comprises mixing MCIP,

XX calcineurin and a test compound -

XX

XX Disclosure; Page 147; 174pp; English.

XX

XX The invention relates to muscle calcineurin interacting proteins (MCIPs)

XX and nucleic acid molecules encoding such proteins. MCIPs form a physical

XX complex with the catalytic subunit of calcineurin and increased levels

XX of MCIPs correspond to a reduced ability of calcineurin to stimulate

transcription of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for treating cardiac hypertrophy and heart failure. Antibodies to MCIP can be used in characterizing the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomyopathy or as predictor of heart disease. The present sequence is human MCIP associated DNA.

Sequence 599 BP; 164 A; 150 C; 149 G; 136 T; 0 other;

Query Match 71.4%; Score 426.2; DB 24; Length 599;
Best Local Similarity 93.1%; Pred. No. 3.4e-118;
Matches 457; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 31 AGCGCCACACCGCTGCCACCTGGACCGCGCGTGTGCTGACGCGCTGTGCGGGCC 90
DB 110 AGCTCCCTGATGCTGTGGTGGCAACGATGATGCTTCAGCGAAGTGAGACCGGGCC 169
QY 91 AAATTTGAATCCCTCTTCAGAACATATGACAAGGACACACCTTCAGTATTTTAAGAGC 150
DB 170 AAATTTGAATCCCTCTTCAGAACATATGACAAGGACACACCTTCAGTATTTTAAGAGC 229
QY 151 TTCAAACGTGCGGATTAACCTTACGACACCCCTTATCTGACGCGATGCCAGGCTGCGG 210
DB 230 TTCAAACGTGCGGATTAACCTTACGACACCCCTTATCTGACGCGATGCCAGGCTGCGG 289
QY 211 CTGCAACAGCGAGTCTCTGGGGAAGAAATGAAGTTGATTTTGTCTCAGACTTTACAC 270
DB 290 CTGCAACAGCGAGTCTCTGGGGAAGAAATGAAGTTGATTTTGTCTCAGACTTTACAC 349
QY 271 ATAGGAAGTTACACCTGGCTCCGCCCAATCCGCAACAGTTCTCATCTCCCTCCG 330
DB 350 ATAGGAAGTTACACCTGGCTCCG-CAATCCGCAACAGTTCTCATCTCCCTCCG 408
QY 331 GCCTCTCTCCGTTGGTGGTGAACAGTAGAAGATGCCACCCCGTCAATAAATACGAT 390
DB 409 GCCTCTCTCCGTTGGTGGTGAACAGTAGAAGATGCCACCCCGTCAATAAATACGAT 468
QY 391 CTTTATATGTCATCTCCAAGCTGGGCGAGGAGAGATGATGAATGATGATGATGATGAT 450
DB 469 CTTTATATGTCATCTCCAAGCTGGGCGAGGAGAGATGATGAATGATGATGATGATGAT 528
QY 451 GACCCCACTCCAGTGTGGTGTCCACGTGTGTGAGAGTGACCAAGAGATGAGGAGAA 510
DB 529 GACACCACTCCAGTGTGGTGTCCACGTGTGTGAGAGTGACCAAGAGATGAGGAGAA 588
QY 511 GAGGAAGAGAT 521
DB 589 GAGGAAGAGAT 599

RESULT 6

AAD30155
ID AAD30155 standard; DNA; 2331 BP.

XX AC AAD30155;

XX DT 17-MAY-2002 (first entry)

XX DE Human MCIP associated DNA #1.

XX KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
XX KW heart failure; cardiomyopathy; heart disease; human; gene; ds.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 144..737
XX FT /*tag= a
XX FT /product= "Human MCIP associated protein #1"

XX PN WO200204491-A2.

XX 17-JAN-2002.

XX 06-JUL-2001; 2001WO-US21662.

XX 07-JUL-2000; 2000US-216601P.

XX 13-FEB-2001; 2001US-0782953.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (WILL/) WILLIAMS S R.

XX (ROTH/) ROTHERMEL B.

XX Williams SR, Rothermel B;

XX WPI; 2002-179698/23.

XX P-PSDB; AAE18914.

Screening for modulators of muscle calcineurin interacting protein (MCIP) binding, expression or phosphorylation, useful for treating cardiac hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a test compound -

Claim 72; Page 155-157; 174pp; English.

The invention relates to muscle calcineurin interacting proteins (MCIPs) and nucleic acid molecules encoding such proteins. MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin to stimulate transcription of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for treating cardiac hypertrophy and heart failure. Antibodies to MCIP can be used in characterizing the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomyopathy or as predictor of heart disease. The present sequence is human MCIP associated DNA.

Note: This sequence has been described as a promoter in claim 72 of the specification, however the sequence seems to be a polynucleotide encoding a MCIP associated protein.

Sequence 2331 BP; 630 A; 470 C; 547 G; 684 T; 0 other;

Query Match 67.6%; Score 403.8; DB 24; Length 2331;

Best Local Similarity 83.2%; Pred. No. 3.7e-111;

Matches 472; Conservative 0; Mismatches 92; Indels 3; Gaps 1;

QY 31 AGCGCCACACCTGCCCTGCCACCTGGACCGCGCGTGTGCGACGCGCTGTGCGGGCC 90

DB 174 AGCTCCCTGATGCTGCTGTGCAACAGTATATCTTCAGCGAAGTGAACCCAGGGCC 233

QY 91 AAATTTGAATCCCTCTTCAGAACATATGACAAGGACACACCTTCAGTATTTTAAGAGC 150

DB 234 AAATTTGAGTCCCTCTTTAGGAGGTATGACAAGGACATCACCTTTTCAGTATTTTAAGAGC 293

QY 151 TTCAAACGTGTCGGGATAAATTCAGCAACCCCTTATCTGACGCGATGCCAGGCTGCGG 210

DB 294 TTCAAACGAGTCAAGATAAATTCAGCAACCCCTTTCGCGCAGCAGATGCCAGGCTCCAG 353

QY 211 CTGCAACAGCCAGTTCCTGGGGAAGAAATGAAGTTGATTTTCTCAGACTTTACAC 270

DB 354 CTGCATTAAGCTGAGTTTCTGGGAAAGAAATGAAGTTATATTTTCTCAGACTTTACAC 413

QY 271 ATAGGAAGTTACACCTGGCTCCGCCCAATFCCGCAACAGATTCCTCATCTCCCTCCG 330

DB 414 ATAGGAAGTCTACACCTGGCTCCGCCCAATFCCGCAACAGATTCCTCATCTCCCTCCG 473

QY 331 GCCTCTCTCCGCTTGGCTGGAAACAAAGTAGAAGATGCCACCCCGTCAATAAATACGAT 390

DB 474 GCCTCTCTCCGCTTGGCTGGAAACAAAGTAGAAGATGCCACCCCGTCAATAAATACGAT 533

QY 391 CTTTATATGCCATCTCCAAGCTGGGGCCAGGAGAGATGATGAATGATGATGATGATGAT 450

DB 534 CTTTATATGCCATCTCCAAGCTGGGGCCAGGAGAGATGATGAATGATGATGATGATGAT 593

Qy 451 GACCCCTCCAGTGTGGTCCACGCTGTGAGAGTGACCAAGAGATGAGGAGAA 510
Db 594 GACACCCTCCAGCGTGGTGGTCCATGTATGTGAGAGTGATCAAGAGAGGAGGAGAA 653
Qy 511 GAGGAAGAGTGGAGAGATGAAGAGACCCCAAGCCCAAAATATCCAGACACGAGACCG 570
Db 654 GAGGAA--ATGGAAGAAATGAGAGACCTTAAGCCAAAATATATCCAGACGAGGCGG 710
Qy 571 GAGTACACACCGATCCACCTTAGCTGA 597
Db 711 GAGTACACGCGGATCCACCTCAGCTGA 737

RESULT 7
ABN96843
ID ABN96843 standard; DNA; 2173 BP.
AC ABN96843;
XX
XX
XX 13-AUG-2002 (first entry)
XX Gene #3341 used to diagnose liver cancer.
XX
XX Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
XX Homo sapiens.
XX
XX WO200229103-A2.
XX
XX 11-APR-2002.
XX 02-OCT-2001; 2001WO-US30589.
XX 02-OCT-2000; 2000US-237054P.
XX (GENE-) GENE LOGIC INC.
XX
XX Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX WPI; 2002-426119/45.
XX
XX Diagnosing and detecting the progression of liver cancer,
PT hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample -
XX
XX Claim 1; SEQ ID NO 3341; 298pp; English.
XX
XX The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN9503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 2173 BP; 606 A; 431 C; 503 G; 633 T; 0 other;

Query Match 66.9%; Score 399.6; DB 24; Length 2173;
Best Local Similarity 87.8%; Pred. No. 6.6e-110;
Matches 448; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

Qy 88 GCCAAATTTGAATCCCTCTTCAGAACATATAGCAAGACACACCCTTCCAGTATTAAAG 147
Db 58 GCCAAATTTGAATCCCTCTTTAGGACCTTATGACAAGACATCATACCTTTTCAATTTAAAG 117
Qy 148 AGCTTCAAACTGCTCCGATATAACTTTCAGCAACCCCTTATCTGCAGCCGATGCCAGGCTG 207
Db 118 AGCTTCAAACTGCTCAGATATAACTTTCAGCAACCCCTTCTCCGACGAGATGCCAGGCTC 177
Qy 208 CGGCTGCACAAAGACGAGTTCCTTGGGGAAGAAATGAAGTTGTATTTTGTCTCAGACTTTA 267
Db 178 CAGCTGCATTAAGACTGAGTTCTTGGGAAAGAAATGAAGTTATATTTTGTCTCAGACCTTA 237
Qy 268 CACATAGGAAGTTTACACCTGCTCCGCCCAATCCCGACAAACAGTTCTCTCATCTCCCT 327
Db 238 CACATAGGAAGTCTACACCTGCTCCGCCCAATCCCGACAAACAGTTCTCTCATCTCCCT 297
Qy 328 CCGGCTCTCTCCCTCGTGGTGGAAACAAGTAGAAGATGCCACCCCGTTCATAAATTTAC 387
Db 298 CCGGCTCTCTCCGCCAGTGGATGGAAACAAGTTGGAAGATGCCACCCAGTTCATAAATTTAT 357
Qy 388 GATCTTTTATATGCCATCTCCAAAGCTGGGGCCAGGAGAGAGTATGAAGTGCATGCAGCG 447
Db 358 GATCTTTTATATGCCATCTCCAAAGCTGGGGCCAGGAGAGTATGAATTCACGACGCG 417
Qy 448 ACAGACCCCTCCAGTGTGGTGTCTCCAGTGTGTGAGAGTGACCAAGAGAAATGAGGAG 507
Db 418 ACTGACACCACTCCAGCTGGTGTGGTGTGTGAGAGTGTGAGAGTGTGAGAGAGGAGGNA 477
Qy 508 GAAGAGGAAGAGATGGAGAGATGAAGAGACCCCAAGCCCAAAATATCTCCAGACGAGGAG 567
Db 478 GAAGAGGAA--ATGGAAGAAATGAGGAGACCTTAAGTCAAAATTTATCCAGACGAGGAG 534
Qy 568 CCGGAGTACACACCGATCCACCTTAGCTGA 597
Db 535 CCGGAGTACACGCGGATCCACCTCAGCTGA 564

RESULT 8
AA01282
ID AA01282 standard; cDNA to mRNA; 2174 BP.
XX
XX AC AA01282;
XX
XX 09-APR-1999 (first entry)
XX Human DSCR1 coding sequence.
XX
XX DSCR1; Down's Syndrome critical region 1; human; pathogenic abnormality;
KW Central Nervous System development; mental retardation; heart defect; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS /..564
FT FT /*tag= a
FT polyA_signal 1541..1546
FT FT /*tag= b
FT polyA_signal 2132..2137
FT FT /*tag= c
XX
XX US5869318-A.
XX
XX 09-FEB-1999.
XX
XX 07-JUN-1996; 96US-0665040.
XX
XX 07-JUN-1995; 95ES-0001140.
XX
XX (PALL/) PALLEJA X E.
XX
XX Fuentes JJ, Palreja xE, Pritchard M;
XX
XX WPI; 1999-152781/13.

Db 601 TGACACCACTCCCGAGCGTGTGGTCCATGATGTGAGAGTGATCAAGAGAGGAGCA 660
Qy 510 AGAGGAAGAGATGAGAGAAATGAAGAGACCCAAAGCCCAAAATCATCCAGACACGGAGACC 569
Db 661 AGAGGAA--ATGGAAGATGAGGAGACCTAAGCCAAAATTTATCCAGACCAAGAGGACC 717
Qy 570 GGAGTACACACCGGATCCACCTTACTGA 597
Db 718 GGAGTACACCGCGATCCACCTCACTGA 745

RESULT 10
AAF25338
ID AAF25338 standard; cDNA; 934 BP.
AC AAF25338;
XX 30-APR-2001 (first entry)
DT Nucleotide sequence of a human detoxification protein.
XX Human; detoxification protein; DETX; cancer; leukaemia; melanoma;
KW adenocarcinoma; autoimmune disorder; inflammatory disorder;
KW rheumatoid arthritis; asthma; atherosclerosis; autoimmune thyroiditis;
KW psoriasis; ulcerative colitis; infection; cell proliferative disorder;
KW actinic keratosis; arteriosclerosis; cirrhosis; hepatitis; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 20..724
FT /*tag= a
FT /product= "detoxification protein"
FT sig_peptide 20..100
FT /*tag= b
XX WO200104305-A2.
XX 18-JAN-2001.
XX 06-JUL-2000; 2000WO-US18509.
XX 07-JUL-1999; 99US-0142678.
XX (INCY-) INCYTE GENOMICS INC.
XX Tang YT, Yue H;
XX WPI; 2001-147193/15.
XX P-PSDB; AAB31788.
XX New human detoxification protein and polynucleotide, useful for
PT diagnosis, prevention and treatment of autoimmune/inflammatory
PT disorders and cell proliferative disorders including cancer -
XX
XX Claim 5; Page 79; 79pp; English.
XX The present sequence encodes a human detoxification polypeptide (DETX).
CC DETX and its (ant)agonists are useful for preventing or treating
CC disorders associated with decreased or increased expression or activity
CC of DETX. DETX polypeptides are useful for screening compounds that
CC specifically binds to DETX and for identifying (ant)agonists.
CC Diseases prevented, treated and diagnosed include cancers (e.g.
CC leukaemia, melanoma, adenocarcinoma, cancers of the brain, bone marrow,
CC breast, kidney, liver, pancreas, prostate and uterus),
CC autoimmune/inflammatory disorders (e.g. rheumatoid arthritis, asthma,
CC atherosclerosis, autoimmune thyroiditis, psoriasis and ulcerative
CC colitis), bacterial, fungal, parasitic infections and cell
CC proliferative disorders (e.g. actinic keratosis, arteriosclerosis,
CC cirrhosis and hepatitis). Anti-DETX antibodies may be used as
CC antagonists, as a targeting or delivery mechanism for bringing
CC pharmaceutical agents into contact with cells or tissues expressing
CC DETX and for diagnosis of DETX-related disorders.

XX SQ Sequence 934 BP; 247 A; 244 C; 206 G; 237 T; 0 other;
Query Match 35.38; Score 211; DB 22; Length 934;
Best Local Similarity 65.28; Pred. No. 3.1e-53;
Matches 332; Conservative 0; Mismatches 165; Indels 12; Gaps 1;
Qy 13 GATCTGCAGGACCTGCCGAGGCCACCATCGCTGCCACCTGGAGCCCGCGGTGTTGGTG 72
Db 143 GACTTCATGACCTCCCACTCGTTGTTGGTGCAATGTTCCACAGCTAGTGTGTTGAA 202
Qy 73 GACGCCCTGTGCCGGGCCAAATTTGAATCCCTCTTCAGAAACATATGACAAGGACACACC 132
Db 203 GGAGAAAGAGAGCAAGGAAATTTGAGGGACTGTTTCGGACTTATGATGACTGTGTGACG 262
Qy 133 TTCCAGTATTTTAAGAGCTTCAAACGTGTCGGGATAAACTTCAGCAACCCCTTATCTGCA 192
Db 263 TTCCAGCTATTTTAAGAGTTTCAGACGTGTCGGTATAACTTCAGCAATCCTAAATCTGCA 322
Qy 193 GCCGATGCCAGGCTCGGCTGCACAAGACCGAGTTCTCTGGGGAAGAAATGAAGTTGAT 252
Db 323 GCCCGAGCTAGGATAGAGCTTCATGAACCCCAATTCAGAGGGGAAAAATTAAGCTCTAC 382
Qy 253 TTGTCTCAGACN-----TTACACATAGGAAGTTACACCTGGCTCCGCCCAAT 300
Db 383 TTGTGCACAGTTTCAGACTCCAGACAGATGGAGACAACTGCACCTTGGCTCCACCCAG 442
Qy 301 CCGGACAAAACAGTTCTCATCTCCGCTCGGCTCTCTCCCTGGTGGTGGGAAACAAGTA 360
Db 443 CCTGCCAAAACAGTTTCTCATCTCGCCCTCTCTCCCTGGTGGGAGGCCCATC 502
Qy 361 GAAGATGCCACCCCGCTCATAAATACGATCTTTATATGCCATCTCCAAGCTGGGGCCA 420
Db 503 AACGATGCCACGCCAGTCTCTCAACTATGACCTCTCTATGCTGTGGCCAACTAGGACCA 562
Qy 421 GGAGAGAAGTATGAACATGCATGCAGCAGACAGACCCCACTCCAGTGTGTGTCCACGTG 480
Db 563 GGAGAGAAGTATGAGTCCATGCAGGAGTGAAGTCCACCCCAAGTGTGTGTCCACGTG 522
Qy 481 TGTGAGAGTACCACAGAGATGAGGAGGA 509
Db 623 TGGACAGTGCATAGAGGAGGAAGAGGA 651

RESULT 11
ABA91457
ID ABA91457 standard; cDNA; 3159 BP.
XX ABA91457;
XX 18-APR-2002 (first entry)
XX Human Down syndrome critical region 1-like 1 protein cDNA.
DE Down syndrome critical region 1-like 1; DSCR1L1 alpha; human;
XX Down syndrome; Alzheimer's disease; dementia; transgenic;
KW neuroprotective; nontropic; anticonvulsant; diagnosis;
KW gene therapy; gene; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 185..952
FT /*tag= a
FT /product= "DSCR1L1"
FT /transl_except= (pos:215..217, aa:Xaa)
FT /note= "Xaa = unknown"
XX WO200204513-A2.
XX 17-JAN-2002.
XX 11-JUL-2001; 2001WO-US21982.
PF

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	515.8	86.4	597	10	US-09-782-953-5
3	481.8	80.7	2212	10	US-09-782-953-14
4	469	78.6	2358	10	US-09-925-302-347
5	426.2	71.4	599	10	US-09-782-953-1
6	403.8	67.6	2331	10	US-09-782-953-11
7	403.8	67.6	2355	12	US-10-044-090-255
8	399.6	66.9	2173	10	US-09-880-107-3340
9	193	32.3	3184	10	US-09-954-456-497
10	193	32.3	3184	10	US-09-782-953-17
11	186.4	31.2	720	10	US-09-782-953-23
12	186.4	31.2	828	10	US-09-782-953-20
13	183	30.7	594	10	US-09-782-953-8
14	144.6	24.2	412	10	US-09-864-761-10388
15	144.6	24.2	446	10	US-09-864-761-2064
16	123	20.6	486	10	US-09-864-761-809
17	91.8	15.4	111	10	US-09-864-761-27019
18	84.4	14.1	123	10	US-09-864-761-17592
19	81.4	13.6	365	10	US-09-728-445-736

c	20	70.6	11.8	85	10	US-09-864-761-18808	Sequence 18808, A
	21	37.8	6.3	2853	10	US-09-965-631-3	Sequence 3, Appli
	22	37.8	6.3	3446	10	US-09-965-631-7	Sequence 7, Appli
	23	36.2	6.1	5739	10	US-09-960-253-142	Sequence 142, App
	24	36.2	6.1	6417	10	US-09-962-436-288	Sequence 288, App
	25	36	6.0	267	10	US-09-923-876-1137	Sequence 1137, Ap
	26	35.6	6.0	490	10	US-09-880-107-2261	Sequence 2261, Ap
	27	34.4	5.8	257	10	US-09-923-876-1928	Sequence 1928, Ap
	28	34.4	5.8	497	10	US-09-822-263-35	Sequence 35, Appl
	29	34.4	5.8	4363	10	US-09-864-864-241	Sequence 241, App
	30	34	5.7	345	10	US-09-822-263-17	Sequence 17, Appl
	31	34	5.7	387	10	US-09-920-300A-395	Sequence 395, App
	32	34	5.7	387	12	US-10-033-528-395	Sequence 395, App
	33	34	5.7	497	10	US-09-822-263-33	Sequence 33, Appl
	34	34	5.7	1147	10	US-09-880-107-2311	Sequence 2311, Ap
	35	33.8	5.7	156	10	US-09-864-761-20014	Sequence 20014, A
	36	33.8	5.7	415	10	US-09-864-761-3236	Sequence 3236, Ap
c	37	33.6	5.6	1752	9	US-09-887-552A-1	Sequence 1, Appli
c	38	33.4	5.6	575	10	US-09-864-761-8864	Sequence 8864, Ap
	39	33.4	5.6	20247	10	US-09-764-877-2680	Sequence 2680, Ap
	40	33.2	5.6	299	10	US-09-864-761-21553	Sequence 21553, A
c	41	33.2	5.6	470	10	US-09-864-761-2442	Sequence 2442, Ap
	42	33.2	5.6	1875	9	US-10-001-835-56	Sequence 56, Appl
c	43	33.2	5.6	2289	10	US-09-850-964-3	Sequence 3, Appli
	44	33	5.5	193	10	US-09-864-761-26305	Sequence 26305, A
	45	33	5.5	466	10	US-09-864-761-5668	Sequence 5668, Ap

ALIGNMENTS

RESULT 1

US-09-782-953-2
; Sequence 2, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674P21
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(594)
US-09-782-953-2

Query Match	100.0%	Score 597;	DB 10;	Length 597;
Best Local Similarity	100.0%	Pred. No. 2.7e-177;		
Matches 597;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGAGAGGAGTGGATCTGCAGGACCTGCGAGCGCCACCATCGCTGCGACCTGGACCG 60		
Db	1	ATGGAGAGGAGTGGATCTGCAGGACCTGCGAGCGCCACCATCGCTGCGACCTGGACCG 60		
QY	61	CCCGTGTTCGTGGAGCGGCTGTGCGGGGCAATTTGAATCCCTCTTCAGACATATGAC 120		
Db	61	CCCGTGTTCGTGGAGCGGCTGTGCGGGGCAATTTGAATCCCTCTTCAGACATATGAC 120		
QY	121	AAGGACACACCTTCCAGTATTTTAAGAGCTTCAACAGTGTCCGGATAAATTCAGCAAC 180		
Db	121	AAGGACACACCTTCCAGTATTTTAAGAGCTTCAACAGTGTCCGGATAAATTCAGCAAC 180		
QY	181	CCCTTATCTGCAGCGGATGCCAGGCTGCGGCTGCACAAGACCGAGTTCCTGGGAGGAA 240		

Db 181 CCTTTATCTGCAGCCGATGCCAGGCTGGGCTGCACAGCAGGATTCCTGGGAGGAA 240
QY 241 ATGAAGTTGATTTTGTCTCAGACTTTACACATAGGAAGTTTACACCTGGCTCCGCCCAAT 300
Db 241 ATGAAGTTGATTTTGTCTCAGACTTTACACATAGGAAGTTTACACCTGGCTCCGCCCAAT 300
QY 301 CCGCACAACAGTTCTCTATCTCCCTCGGGCTCTCTCTCCCTGGTGGTGGGAAACAGTA 360
Db 301 CCGCACAACAGTTCTCTATCTCCCTCGGGCTCTCTCTCCCTGGTGGTGGGAAACAGTA 360
QY 361 GAAGATGCCACCCCTGATATAATACGATCTTTATATGCGCATCTCCAAGCTGGGGCA 420
Db 361 GAAGATGCCACCCCTGATATAATACGATCTTTATATGCGCATCTCCAAGCTGGGGCA 420
QY 421 GGAGAGAAGTATGAATGCTGACGAGCAGACGCGGAGTTCACACCTCCACCTTACGCTG 480
Db 421 GGAGAGAAGTATGAATGCTGACGAGCAGACGCGGAGTTCACACCTCCACCTTACGCTG 480
QY 481 TGTGAGAGTGACCAAGAGATGAGGAGGAGGAGGAGGAGATGAGAGATGAGAGACCC 540
Db 481 TGTGAGAGTGACCAAGAGATGAGGAGGAGGAGGAGGAGATGAGAGATGAGAGACCC 540
QY 541 AAGCCCAAAATCATCCAGACGAGACCGGAGTTCACACCTCCACCTTACGCTG 597
Db 541 AAGCCCAAAATCATCCAGACGAGACCGGAGTTCACACCTCCACCTTACGCTG 597

RESULT 2
US-09-782-953-5
; Sequence 5, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: UTSD:674P21
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(594)
US-09-782-953-5

Query Match 86.4%; Score 515.8; DB 10; Length 597;
Best Local Similarity 94.4%; Pred. No. 7.4e-152;
Matches 535; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 31 AGCGCCACCATCGCTGCCACCTGGACCGCGGCTGTTCGTGGACGCGCTGTGCCGGGCC 90
Db 31 AGCTCCCTGTGTTGTGTGGCAACAGATGATGCTTCACGGAAGTGGAGACCGGCC 90
QY 91 AAATTTGAATCCCTTTCAGAACATATGACAAAGGACACCACTTCCAGATATTTAAAGC 150
Db 91 AAATTTGAATCCCTTTCAGAACATATGACAAAGGACACCACTTCCAGATATTTAAAGC 150
QY 151 TTCAACGTGTCGGGATAAACTTACGACCCCTTATCTGACGCGGATGCCAGGCTCGG 210
Db 151 TTCAACGTGTCGGGATAAACTTACGACCCCTTATCTGACGCGGATGCCAGGCTCGG 210
QY 211 CTGCACAAGACCGAGTTCTTCTGGGAGGAAATGAAGTTGATTTTGTCTCAGACTTTAC 270
Db 211 CTGCACAAGACCGAGTTCTTCTGGGAGGAAATGAAGTTGATTTTGTCTCAGACTTTAC 270

QY 271 ATAGGAAGTTTACACCTGGCTCCGCCCAATCCCGACAAACAGTTTCTCATCTCCCTCCG 330
Db 271 ATAGGAAGTTTACACCTGGCTCCGCCCAATCCCGACAAACAGTTTCTCATCTCCCTCCG 330
QY 331 GCCTCTCTCCCTGGTGGTGAACAGTAGAAGTGCACCCCGCTCATATAAATTACGAT 390
Db 331 GCCTCTCTCCCTGGTGGTGAACAGTAGAAGTGCACCCCGCTCATATAAATTACGAT 390
QY 391 CTTTATATGCACTCCCAAGCTGGGCGAGGAGAGATATGAATGCAATGCATGCAGCGACA 450
Db 391 CTTTATATGCACTCCCAAGCTGGGCGAGGAGAGATATGAATGCAATGCATGCAGCGACA 450
QY 451 GACCCCACTCCCAAGTGTGTGTCACGTGTGTGAGAGTGACCAAGAGAAATGAGAGGAA 510
Db 451 GACCCCACTCCCAAGTGTGTGTCACGTGTGTGAGAGTGACCAAGAGAAATGAGAGGAA 510
QY 511 GAGGAAGAGATGGAGAGATGAAGAGACCCCAAGCCCAAAATCATCCAGACGAGACCG 570
Db 511 GAGGAAGAGATGGAGAGATGAAGAGACCCCAAGCCCAAAATCATCCAGACGAGACCG 570
QY 571 GAGTACACACCGATCCACCTTAGCTGA 597
Db 571 GAGTACACACCGATCCACCTTAGCTGA 597

RESULT 3
US-09-782-953-14
; Sequence 14, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: UTSD:674P21
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 2212
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(615)
US-09-782-953-14

Query Match 80.7%; Score 481.8; DB 10; Length 2212;
Best Local Similarity 89.1%; Pred. No. 7.1e-141;
Matches 532; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 1 ATGAGGAGGTGGATCTGCAGGACCTGCCGAGCGCCACCATCGCTCCACCTGGACCCG 60
Db 25 ATGAGGAGGTGGATCTGCAGGACCTGCCGAGCGCCACCATCGCTCCACCTGGACCCG 84
QY 61 CGCGTGTTCGTGACGCGCTGTGCCGGGCAATTTGAATCCCTTTCAGAACATATGAC 120
Db 85 CGCGTGTTCGTGACGCGCTGTGCCGGGCAATTTGAATCCCTTTCAGAACATATGAC 144
QY 121 AAGGACACCACTTCCAGTATTTTAAAGCTTCAAAAGCTGTCCGGATTAACCTTCAGCAAC 180
Db 145 AAGGACATACCTTTCAGTATTTTAAAGCTTCAAAAGCTGTCCGGATTAACCTTCAGCAAC 204
QY 181 CCCTTATCTGACGCGATGCCAGCTGCGCTGCACAAAGACCGAGTTCTTGGGAGGAA 240
Db 205 CCCTTCTCCGAGCAGATGCCAGCTCCAGCTGCATAAGACTGAGTTTCTTGGGAAAGAA 264
QY 241 ATGAAGTTGATTTTGTCTCAGACTTTACACATAGGAAGTTTACACCTGGCTCCGCCCAAT 300
Db 265 ATGAAGTTATTTTGTCTCAGACTTTACACATAGGAAGTTTACACCTGGCTCCGCCCAAT 324

Qy	301	CCCGACAAACAGTTCCTCCTCCCTCCGGCCCTCTCCCTCCGTTGGCTGGAAACAAGTA	360
Db	325	CCAGAACAGCAGTTTCTGATCTCCCTCCCGCTCTCCGCGAGTGGATGGAACAAGTG	384
Qy	361	GAAGATGCCACCCCGGTCATAAATACGATCTTTTATATGCCATCTCCAAAGCTGGGGCCA	420
Db	385	GAAGATCGACCCCGTCATAAATATGATCTCTTATATGCCATCTCCAAAGCTGGGGCCA	444
Qy	421	GGAGAGAAGTATGAATGCGATCAGCGGACAGACCCCACTCCCAAGTGTGGTGTCCACAGTG	480
Db	445	GGGAAAAGTATGAATTGTCACGACGCGACTGACACCACTCCCAAGCGTGTGTGTCCTATGA	504
Qy	481	TGTGAGAGTGCACCAAGAGAATGAGGAGGAAGACGAAGATGAGAGAATGAAGACGCC	540
Db	505	TGTGAGAGTGTCAAGAGAGGAGGAAGACAGAA---ATGGAAGAATGAGGAGACCT	561
Qy	541	AAGCCCAAAATCATCCAGACACGGAGACCGGATACACACCGATCCACCTTAGCTGA	597
Db	562	AAGCAAAAATATTCAGACACGAGGCGCGGATACACGCGATCCACCTCAGCTGA	618

RESULT 4

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US-09-925-302-347
; Sequence 347, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 347
; LENGTH: 2358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-302-347

```

Query Match	78.6%;	Score 469;	DB 10;	Length 2358;
Best Local Similarity	88.6%;	Pred. No. 7.6e-137;		
Matches 529;	Conservative 2;	Mismatches 62;	Indels 4;	Gaps
Qy 1	ATGGAGGAGGTGGATCTGCAGGACCTTGC	CGCAGCGCCACCATCGCTTGCACCTTGGACCCG	60	
Db 114	ATGGAGGAGGTGGACCTTGCAGGACCTGCC	CAGCGCCACCATCGCTTGCACCTGGACCCG	173	
Qy 61	CGCGTGTCTGTGGACGCCCTGTGCGGGGCC	AAATTTTGATCCCTCTTCAGAACATATGAC	120	
Db 174	CGCGTGTCTGTGGACGCCCTGTGCGGGGCC	AAATTTTGATCCCTCTTCAGAACATATGAC	233	
Qy 121	AAGCACACCACTTCCAGTATTTTAAGAGCTT	CAACAGGTGTCGGATAAACTTTCAGCAAC	180	
Db 234	AAGCACATCACTTTTCAGTATTTTAAGAGCTT	CAACAGGTGTCAGATAAACTTTCAGCAAC	293	
Qy 181	CCCTTATCTCGACCGGATGCCAGGCTCGCGG	CTGCACAGACCAAGTTCCTGGGGAAGGAA	240	
Db 294	CCCTTCTCCGACAGATGCCAGGCTCCAGCTC	GCATAAAGACTCAGTTCCTGGGAAAAGAA	353	
Qy 241	ATGAAGTGTGATTTTGTCTCAGACTTTACAT	ATAGGAAGTTTCACACCTGGCTCGGCCCAAT	300	
Db 354	ATGAAGTGTATTTTGTCTCAGACTTTACAT	ATAGGAAGTTTCACACCTGGCTCGGCCCAAT	412	
Qy 301	CCCGCAACAGACTTCCTCATCTCCCTTC	CGGCTCTCTCTCCCTTGGCTGGGAACAAGTA	360	
Db 413	CCAGCAAGCAGGTTTCTGATCTCCCTTC	CGGCTCTCTCCGSCAGTGGGATGGAACAAGTG	472	
Qy 361	GAAGATGCCACCCCGGTCATAAAATTCGATCT	TTTTATATGCCATCTCCCAAGCTGGGGCCA	420	

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Db 473 GAAGATGGACCCAGTCATAAATATATGATCTTATATGCCATCTCCAAGCTGGGGCCA 532
QY 421 GGAGAGAAGTATGAATCATGCGACGACACCCCACTCCCACTGGTGGTCCACGCTG 480
Db 533 GGGGAAAGTATGAATTCACGACGCACTGCACCACTCCCAAGCTGGTGCCTCATGTA 592
QY 481 TGTGAGAGTGACCAAGAGAAGTATGAGGAGGAAGAGAGATGGAGAGAGAAATGAAGAGACCC 540
Db 593 TGTAGAGTGTATCAAGAGAAGGAGGAAGAGAGGAAA---ATGGAAGAAATGAGGAGACCT 649
QY 541 AAGCCCAAAATCATCCACACGAGACCGGAGTACACACCGATCCACCTTAGCTGA 597
Db 650 AAGCCAAAAATATTCACACGAGGAGCGGAGTACAGCCGATCCACCTCAGCTGA 706

RESULT 5
US-09-782-953-1
; Sequence 1, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674P21
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-782-953-1

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RESULTS

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US-09-782-953-1
; Sequence 1, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674P21
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-782-953-1

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Query Match	71.4%	Score 426.2	DB 10	Length 599
Best Local Similarity	93.1%	Prod. No. 8.7e-124		
Matches 457	Conservative 0	Mismatches 33	Indels 1	Gaps 1
QY	31	ACGCCACCATCGCTGCCACCTGACCCGGCGGTTCGTGTGGAGGGCCTGTGCCGGGCC	90	
Db	110	AGCTCCCTCGATGTCTGTGTGCAACACGATGATGCTTCACGGAAGATGACACGAGGCC	169	
QY	91	AAATTTGAACTCCCTTCAGAACATATCACAAGACACACCTCTCCACGATATTTTAAAGAGC	150	
Db	170	AAATTTGAACTCCCTTCAGAACATATGACAAGACACACCTCTCCACGATATTTTAAAGAGC	229	
QY	151	TTCAACAGCTGTCCGGATAAACCCTTCAGCAACCCCTTATCTGCAGCCGATGCCAGGCTGCGG	210	
Db	230	TTCAACAGCTGTCCGGATAAACCCTTCAGCAACCCCTTATCTGCAGCCGATGCCAGGCTGCGG	289	
QY	211	CTGCACAAGACCGAGTTCCCTGGGGAAGAAATGAAGTTGTATTTTGTCTCAGACATTTACAC	270	
Db	290	CTGCACAAGACCGAGTTCCCTGGGGAAGAAATGAAGTTGTATTTTGTCTCAGACATTTACAC	349	
QY	271	ATAGAAGTTTACACACTGGCTCCGCCCAATCCCGACAACAGTAGTTCCTCATCTCCCTCCG	330	
Db	350	ATAGAAGTTTACACACTGGCTCCG-CCAATCCCGACAACAGTAGTTCCTCATCTCCCTCCG	408	
QY	331	GCCTCTCTCCGTTGGCTTGGAAACAAGTAGAAGATGCCACCCCGTCATAAATTACGAT	390	
Db	409	GCCTCTCTCCGTTGGCTTGGAAACAAGTAGAAGATGCCACCCCGTCATAAATTACGAT	468	
QY	391	CTTTTATATGCCATCTCCAAGCTGGGGCCAGGAGAGAAGTAGTAACCTGCATGCAGCGACA	450	
Db	469	CTTTTATATGCCATCTCCAAGCTGGGGCCAGGAGAGAAGTAGTAACCTGCATGCAGCGACA	528	
QY	451	GACCCCACTCCCAAGTGTGGTGTCCACGTGTGTGAGATGTACCAAGAGAATGAGGAGGAA	510	
Db	529	GACCACTCCCAAGTGTGGTGTCCACGTGTGTGAGATGTACCAAGAGAATGAGGAGGAA	588	

RESULT 8
US-09-880-107-3340
; Sequence 3340, Application US/09880107
; Patent No. US20020142981A1

Db 696 AGAGGAAGAAGGA 710

RESULT 10
US-09-782-953-17
; Sequence 17, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS

```

; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: US/09/782,953
; CURRENT APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 3184
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (205)..(780)
US-09-782-953-17

Query Match      32.3%; Score 193; DB 10; Length 3184;
Best Local Similarity 67.4%; Pred. No. 2.7e-50;
Matches 293; Conservative 0; Mismatches 130; Indels 12; Gaps 1;

QY 87 GGCACAAATTTGAATCCCTCTTCAGAACATATGACAAAGGACACACCCTTCCAGTATTTTAA 146
Db 276 GGAATAATTTGGGGACTGTTTCGGACTTATGATGACTGTGTGACGTTTCCAGCTATTTAA 335

QY 147 GAGCTTCAAACGTCGCGGATAAATCTTCAGAACCCCTTATCTGCAGCCGATGCCAGCT 206
Db 336 GAGTTTCAGAGCTGTCGCTATATAAATCTCAGCAATCCTAAATCTGCAGCCGAGCTAGGAT 395

QY 207 GCGGCTGCACAAGACCGAGTTCCTGGGGAAGAAATGAAGTTGTATTTTGTCTCAGACT-- 264
Db 396 AGAGCTTCATGAACCCCAATTCAGAGGGAATAAATTAAGCTCTACITTTGCACAGGTTC 455

QY 265 -----TTACACATAGGAAGTTACACCTGGCTCGGCCCAATCCCGCAACAAGATT 314
Db 456 GACTCCAGAGACAGATGGAGACAACACTGCACCTGGCTCCACCCAGCGCTGCCAACAAGTT 515

QY 315 CTTGATCTCCCTCCGCGCTCTCTCCCGTTGGTGGGAAACAAGTAGAAGATGCCACCC 374
Db 516 TCTATCTCGCCCCCTCTCTCCACCTGTTAGCTGGGACCCCATCAACGATGCCACGCC 575

QY 375 CGTCATAAATTACGATCTTTATATGCCATCTCCAACTGCGGCCGAGGAGAGATATGA 434
Db 576 ACTCTCAACTATGACCTCTCTATGCTGTGGCCAACTAGGACACGAGGAGAGATATGA 635

QY 435 ACTGATGACGAGCAGACACCCCACTCCAGTGTGGTGTCCACGTTGTGTGAGTGAACCA 494
Db 636 GCTCCATGCGAGGACTGAGTCCACCCCAAGTGTGCTGTCGACGTTGCGGACAGTGACAT 695

QY 495 ACAGATGAGGAGGA 509
Db 696 AGAGGAAGAAGAGGA 710

RESULT 11
US-09-782-953-23
; Sequence 23, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: US/09/782,953
; CURRENT APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23

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; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(637)
US-09-782-953-23

Query Match      31.2%; Score 186.4; DB 10; Length 720;
Best Local Similarity 62.6%; Pred. No. 1.3e-48;
Matches 317; Conservative 0; Mismatches 171; Indels 18; Gaps 1;

QY 4 GAGGAGGTGGATCTGCAGACCTGCGGAGCGCCAGCCATCGCTGCCACTTGCACCGCGC 63
Db 56 GAGATGATGGATTAAAGTATGATCTGCTACCTCACTTTTGTGACGCTCCATGAAGA 115

QY 64 GTGTTCTGTCAGCGGCTGTGCGGGCCCAATTTGAATFCCCTCTTCAGAACATATGACAAG 123
Db 116 GTGTTTGGAGCAGGAGAGGAAAGATTGGAAGCACTCTTCCACCATCTATGATGAC 175

QY 124 GACACCACCTTCCAGTATTTTAAAGACTTCAAAACGTTGTCGGGATAAACTTCAGCAACCCC 183
Db 176 CAGTTTACITTTTCAGCTGTTTAAAGCTTTAGAAGAGTCAGATAAATTTTCAGCAACCT 235

QY 184 TTATCTGCAGCCGATGCCAGGCTGCGGCTGCACAAACCGAGTTCTCTGGGAGGAATG 243
Db 236 GAAGCGCGCAGAGAGCGCAATAGAACTCCACGAAACAGACTTCAATGGGCGAGAGCGAA 295

QY 244 AAGTTGATTTTCTCAGACTTTTACACATAGGAAGTTTACACCTGGCTCCGCCCAATCCC 303
Db 296 AAGCTATTTTTCACAG-----TCTATCTCTCGCGCCCGCCAGCT 337

QY 304 GACAAACAGTTCTCATCTCCCTCCGCGCTCTCTCCCGCTCTCTCCCGCTGGCTGGAAACAAGTAGAA 363
Db 338 GTCAAGCAGTTCTCATCTCCCTCCAGCTCTCCCGCTGGGCTGGGAGAGAGAGCGAA 397

QY 364 GATGCCACCCCTCATATAAATTAGATCTTTTATATGCCATCTCCAAGCTGGGCGCCAGGA 423
Db 398 GATGCGATGCTGTATATAAATTAGATTTACTCTGTGCTGTTTCCAAATTTGGGACCCAGGA 457

QY 424 GAGAAGTATGAACATGTCATGCGAGCAGACAGACCCCACTCCCACTGTTGGTGTCCAGGTGTGT 483
Db 458 GAGAAATATGAACITTCACGCGGGAACAGAGTCGACAGCCAGCGTGGTGTTCATGCTGT 517

QY 484 GAGAGTACCAAGAGATGAGGAGGA 509
Db 518 GAAAGTGAACCTGAAGAGGAAGAAGA 543

RESULT 12
US-09-782-953-20
; Sequence 20, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: US/09/782,953
; CURRENT APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23)..(745)
US-09-782-953-20

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Query Match	31.28;	Score 186.4;	DB 10;	Length 828;
Best Local Similarity	61.8%;	Pred. No. 1.4e-48;		
Matches 320;	Conservative 0;	Mismatches 186;	Indels 12;	Gaps 1;
Qy 4	GAGGAGGTGGATCTGCAGGACCTGCCGAGCGCCACCATCGCTGCCACCTGGACCCGGGC	63		
Db 134	GAGATGATGGATTTAAAGTGATTCGCTACCTCACTTTTGTTCGAGCGTCCATGAAGCA	193		
Qy 64	GTGTTCTGTGGACGGCTGTGCGGGCCAAATTTGAATCCCTCTTTCAGAAACATATGACAAG	123		
Db 194	GTGTTTGAGGCACAGAGCAGAGAAGAAAGATTTGAAGCACTCTTCACCATCTATGATGAC	253		
Qy 124	GACACCACCTTCCAGTATTTTAAAGAGCTTCAAACTGTGTCGGATAAACTTCAGCAACCCC	183		
Db 254	CAGGTTACTTTTTCAGCTGTTTAAAAAGCTTTAGAAGAGTCAGAATAAAATTTTCAGCAAACT	313		
Qy 184	TTATCTGACCGGATGCCAGCTCGGGCTGCACAAGACCCGAGTTCCTGGGGAAAGAAATG	243		
Db 314	GAAGCGGCAGCAAGCGCGGAATAGAATCCACGAAACAGACTTCAATGGCGCAAGGCTA	373		
Qy 244	AAGTTGATTTTGTCTCAAG-----ACTTTACACATAGGAAGTTTCACACTGGCT	291		
Db 374	ANGCTATATTTGCACAGGTCGATGTCGGCGAAGTGCGGGACAGCTCTATCTCCTG	433		
Qy 292	CCGCCCAATCCGACAAACAGTTCCCTCATCTCCCTCCGGCTCTCCTCCCGTTGGCTGG	351		
Db 434	CCGCCCAAGCCTGCAAGCAGTTCTCTATCTCCCTCCAGCCTCTCCCCAGTGGGGTGG	493		
Qy 352	AAACAAGTAGAAGATGCCACCCCGTCAATAAATTACGATCTTTTATATGCCATCTCCAAG	411		
Db 494	AAGCAGAGCAGGAATGGGATGCCCTGTTTATAAATTATGATTTACTGTGTGCTTCCAAA	553		
Qy 412	CTGGGGCCAGGAGAGAAGTATGAAGTGCATCGCAGCAGACCCCACTCCCAAGTGTGGTG	471		
Db 554	TTGGACCAAGGAGAAATATGAATCTCACGGGGAACAGAGTCGACACCCAGCGTGTG	613		
Qy 472	GTCCACGTGTGTGAGGTGACCAAGAGAAATGAGGAGGA	509		
Db 614	GTTCATGTCTGTGAAGTGAACCTGAAGGAGGAAGAAGA	651		

```

RESULT 13
US-09-782-953-8
: Sequence 8, Application US/09782953
: Patent No. US20020150953A1
: GENERAL INFORMATION:
: APPLICANT: WILLIAMS, R. SANDERS
: APPLICANT: ROTHERMEL, BEVERLY
: TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
: FILE REFERENCE: US/09-782-953
: CURRENT APPLICATION NUMBER: US/09/782,953
: CURRENT FILING DATE: 2001-02-13
: PRIOR APPLICATION NUMBER: 60/216,601
: PRIOR FILING DATE: 2000-07-07
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: PatentIn Ver.. 2.1
: SEQ ID NO 8
: LENGTH: 594
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(591)
US-09-782-953-8

Query Match 30.7%; Score 183; DB 10; Length 594;
Best Local Similarity 61.7%; Pred. No. 1.4e-47;
Matches 341; Conservative 0; Mismatches 185; Indels 27; Gaps 2;

QY 41 TCGCCTGCCACTGGACCGCGTTCGTGGACGGCCTGTGCGGGCCCAATTGTAAT 100
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[illegible]

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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10388
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000054.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.62
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.67
US-09-864-761-10388

Query Match 24.2%; Score 144.6; DB 10; Length 412;
Best Local Similarity 89.1%; Pred. No. 1.2e-35;
Matches 156; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 87 GGCCTCAAGACCGAGTTCCTGGGGAAGGAATGAAGTTGATTTTCTCAG 261
Db 411 GGCCAAATTTGAATCCCTCTTCAAGACATATGACAGGACACCCATCCAGTATTTAA 146
QY 147 GAGCTTCAACAGTGTCCGGATAAACTTCAGAACCCCTTATCTGCAGCCCATGCCAGGCT 206
Db 351 GAGCTTCAACAGGAGTCAAGTAACTTCAGAACCCCTTCTCCGACGACATGCCAGGCT 292
QY 207 GCGCTGCACAGACCGAGTTCCTGGGGAAGGAATGAAGTTGATTTTCTCAG 261
Db 291 CCAGCTGCATAAGACTGAGTTCTTGGGAAGGAATGAAGTTATATTTTCTCAG 237

RESULT 15
US-09-864-761-2064/c
; Sequence 2064, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 2064
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000122.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
US-09-864-761-2064
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Query Match 24.2%; Score 144.6; DB 10; Length 446;
Best Local Similarity 89.1%; Pred. No. 1.2e-35;
Matches 156; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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QY 87 GGCCAAATTTGAATCCCTCTTCAAGACATATGACAGGACACCCATCCAGTATTTAA 146
Db 445 GGCCAAATTTGAGTCCCTCTTTAGGACGATGACAAAGGACATCACCTTTTCAGTATTTAA 386
QY 147 GAGCTTCAACAGTGTCCGGATAAACTTCAGAACCCCTTATCTGCAGCCCATGCCAGGCT 206
Db 385 GAGCTTCAACAGGAGTCAAGTAACTTCAGAACCCCTTCTCCGACGACATGCCAGGCT 326
QY 207 GCGCTGCACAGACCGAGTTCCTGGGGAAGGAATGAAGTTGATTTTCTCAG 261
Db 325 CCAGCTGCATAAGACTGAGTTCTTGGGGAAGGAATGAAGTTATATTTTCTCAG 271
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Search completed: November 15, 2002, 03:31:14
Job time : 57 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2002, 01:34:13 ; Search time 1973 seconds
(without alignments)
4900.510 Million cell updates/sec

Title: US-09-575-580B-2
Perfect score: 597
Sequence: 1 atggaggagggtgctgca.....caccgatccaccttagctga 597

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpi:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	518.4	86.8	520	14	BQ749142
2	507.8	85.1	1158	14	BQ895506
3	506.2	84.8	1507	11	AK010696
4	495.6	83.0	753	13	B1148584
5	481.8	80.7	890	9	AL538796
6	481.4	80.6	828	9	AL536447

7	476.6	79.8	956	9	AL556803
8	471.4	79.0	937	12	BE795722
9	469.2	78.6	867	14	BQ427531
10	468.6	78.5	923	9	AL551657
11	465.4	78.0	711	13	BG915568
12	463.4	77.6	950	12	BG296537
13	461.4	77.3	980	12	BG296537
14	461.2	77.3	665	13	B1219142
15	453	75.9	710	10	B8617325
16	445	74.5	827	13	B1102432
17	439.2	73.6	727	13	B1327875
18	426.2	71.4	599	9	AA200984
19	409	68.5	570	10	BE287582
20	405.4	67.9	837	9	AU124628
21	403.8	67.6	939	9	AL546617
22	403.8	67.6	1041	13	BM450020
23	402.8	67.5	718	9	AU131040
24	402.2	67.4	931	9	AL543576
25	401.6	67.3	1014	9	AL559594
26	400.6	67.1	946	14	BQ278576
27	400.4	67.1	875	12	BG574693
28	399	66.8	939	9	AL554686
29	393.8	66.0	740	13	B1463566
30	392.8	65.8	885	9	AL544755
31	391	65.5	906	9	AL544313
32	385.2	64.5	769	13	B1767955
33	383.4	64.2	662	13	B1464521
34	378.6	63.4	1078	13	BM541636
35	367	61.5	710	12	BG475986
36	365.8	61.3	811	12	BG570239
37	364.6	61.1	751	9	AL576189
38	360.4	60.4	526	10	AW957479
39	356.8	59.8	627	13	B1859506
40	354.8	59.4	501	12	BF385073
41	354	59.3	600	14	BM743740
42	351	58.8	400	9	AL362314
43	340.6	57.1	437	10	AW291822
44	337.4	56.5	705	9	AL550372
45	336.2	56.3	1047	12	BG287042

ALIGNMENTS

RESULT 1
LOCUS BQ749142 520 bp mRNA linear EST 17-JUL-2002
DEFINITION UI-M-FD0-byd-c-04-0-UI.r1 NIH-BMAP_FD0 Mus musculus cDNA clone
IMAGE:5716539 5', mRNA sequence.
ACCESSION BQ749142
VERSION BQ749142.1 GI:21895929
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 520)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
(BMAP)
This clone was contributed by the Brain Molecular Anatomy Project
Seq primer: pyx-5.
Location/Qualifiers

Query Match	84.8%;	Score 506.2;	DB 11;	Length 1507;
Best Local Similarity	99.4%;	Pred. No. 2.8e-124;		
Matches 508;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

87 GGCAAAATTTGAATCCCTCTTCAGACATATGACAGGACACACCTTCAGTATTTTAA 146
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54 GGCAAAATTTGAATCCCTCTTCAGACATATGACAGGACACACCTTCAGTATTTTAA 113
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147 GAGCTTCAAAAGCTGTCGGGATAACTTCAGCAACCCCTTATCTGCGAGCCGATGCCAGGCT 206
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114 GAGCTTCAAAAGCTGTCGGGATAACTTCAGCAACCCCTTATCTGCGAGCCGATGCCAGGCT 173
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207 GCGGCTGCACAAGACCGAGTTCCTTGGGGAAGGAATGAAGTTGTATTTTCTCAGACTTT 266
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174 GCGGCTGCACAAGACCGAGTTCCTTGGGGAAGGAATGAAGTTGTATTTTCTCAGACTTT 233
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267 ACACATAGGAAGTTACACCTGGCTCGGCCAATCCGCAACACAGTTCCTCATCTCCC 326
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234 ACACATAGGAAGTTACACCTGGCTCGGCCAATCCGCAACACAGTTCCTCATCTCCC 293
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327 TCCGGCTCTCCTCCGTTGGCTGGAACAAAGTAGAAGATGCCACCCCGTCTATAAATTA 386
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294 TCCGGCTCTCCTCCGTTGGCTGGAACAAAGTAGAAGATGCCACCCCGTCTATAAATTA 353
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387 CGATCTTTTATATGCCATCTCCAGCTGGGCGCAGGAGAGATGATGAATGCATGAGC 446
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354 CGATCTTTTATATGCCATCTCCAGCTGGGCGCAGGAGAGATGATGAATGCATGAGC 413
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447 GACAGACCCCACTCCAGTGTGGTCCAGCTGTGTGAGAGTGACCAAGAGAAATGAGGA 506
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414 GACAGACCCCACTCCAGTGTGGTCCAGCTGTGTGAGAGTGACCAAGAGAAATGAGGA 473
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507 GGAAGAGGAAGAGATGGAGAGAAATGAAGAGACCCCAAGCCCAAAATCATCCAGACCGAG 566
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474 GGAAGAGGAAGAGATGGAGAGAAATGAAGAGACCCCAAGCCCAAAATCATCCAGACCGAG 533
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567 ACCGGAGTACACCGATCCACCTTAGCTGA 597
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534 ACCGGAGTACACCGATCCACCTTAGCTGA 564
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LOCUS 602911995F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5053246 5',
DEFINITION mRNA sequence.
ACCESSION B1148584
VERSION B1148584.1 GI:14608585
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 753)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1144 row: m column: 23
High quality sequence stop: 751.
Location/Qualifiers
1. 753
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5053246"
/clone.lib="NCI_CGAP_L19"
/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: liver; Vector: pCMV-SPORT6; Site1: NotI;
Site2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 207 a 197 c 192 g 157 t
ORIGIN
Query Match 83.0%; Score 495.6; DB 13; Length 753;
Best Local Similarity 99.0%; Pred. No. 1.4e-121;
Matches 509; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 84 CCGGGCCAAATTTGAATCCCTCTTCAGACATATGACAGGACACACCTTCAGTATTTT 143
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Db 171 CCAGGCCAAATTTGAATCCCTCTTCAGACATATGACAGGACACACCTTCAGTATTTT 230
|||
QY 144 TAGAGCTTCAACAGCTGTCGGGATAACTTCAGCAACCCCTTATCTGCGAGCCGATGCCAG 203
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Db 231 TAAGAGCTTCAACAGCTGTCGGGATAACTTCAGCAACCCCTTATCTGCGAGCCGATGCCAG 290
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QY 204 GCTGCGGCTGCACAAGACCGAGTTCCTTGGGGAAGGAATGAAGTTGTATTTTCTCAGAC 263
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Db 291 GCTGCGGCTGCACAAGACCGAGTTCCTTGGGGAAGGAATGAAGTTGTATTTTCTCAGAC 349
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QY 264 TTTACATAGGAAGTTACACCTGGCTCGGCCAATCCGCAACACAGTTCCTCATCTC 323
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Db 350 TTTACATAGGAAGTTACACCTGGCTCGGCCAATCCGCAACACAGTTCCTCATCTC 409
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QY 324 CCCTCGGCGCTCTCCTCCCGTTGGCTGGAACAAAGTAGAAGATGCCACCCCGTCTATAA 383
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Db 410 CCCTCGGCGCTCTCCTCCCGTTGGCTGGAACAAAGTAGAAGATGCCACCCCGTCTATAA 469
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QY 384 TTACGATCTTTTATATGCCATCTCCAGCTGGGCGCAGGAGAGATGATGAATGCATGTC 443
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Db 470 TTACGATCTTTTATATGCCATCTCCAGCTGGGCGCAGGAGAGATGATGAATGCATGTC 529
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QY 444 AGGACAGACCCCACTCCAGTGTGGTCCAGCTGTGTGAGAGTGACCAAGAGAAATGA 503
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Db 530 AGGACAGACACCACTCCAGTGTGGTCCAGCTGTGTGAGAGTGACCAAGAGAAATGA 589
|||
QY 504 GGAGGAAGAGAGAGATGGAGAGATGAAGAGACCCCAAGCCCAAAATCATCCAGACAGC 563
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Db 590 GGAGGAAGAGAGAGATGGAGAGATGAAGAGACCCCAAGCCCAAAATCATCCAGACAGC 649
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QY 564 GAGACCGGAGTACACCGATCCACCTTAGCTGA 597
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Db 650 GAGACCGGAGTACACCGATCCACCTTAGCTGA 683
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RESULT 5
AL538796
LOCUS AL538796 LTI_FL013_FBrnl Homo sapiens cDNA clone CS0DF037YL22 5
DEFINITION prime, mRNA sequence.
ACCESSION AL538796
VERSION AL538796.1 GI:12867423
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 890)
Li, W.H., Gruber, C., Jesses, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 890
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DF037YL22"

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week, 24 week and 26 week)
/lab_host="DH10B"
/notes="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dt) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville,
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      194 a      235 c      261 g      137 t      1 others
ORIGIN
Query Match      80.6%; Score 481.4; DB 9; Length 828;
Best Local Similarity 88.9%; Pred. No. 9.le-118;
Matches 531; Conservative 1; Mismatches 62; Indels 3; Gaps 1;

Qy      1  ATGAGAGAGGTGGATCTGCAGGACCTGCGAGCGCCACCACCATCGCGTGCACCTCGACCCG 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      216 ATGAGAGAGGTGGACCTGTCAGGACCTGCGCCAGCGCCACCACCATCGCGTGCACCTCGACCCG 275

Qy      61  CGCGTGTTCTGTGGAGCGCTCTGCGCGGCCAAATTTGAATCCCTTCTCAGAACATATATGAC 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      276 CGCGTGTTCTGTGGAGCGCTCTGCGCGGCCAAATTTGAGTCCCTTCCTTAGACGATATGAC 335

Qy      121 AAGGACACCACCTTCCAGTATTTTAAAGAGCTTCAAAGCTGTCCGGATAAACCTTCAGCAAC 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      336 AAGGACATCACCTTTCAGTATTTTAAAGCTTCAAAGAGTCAGATAAACTTCAGCAAC 395

Qy      181 CCCTTATCTGCAGCGGATGCCAGGCTGGGGCTGCACAAGACCGAGTTCCTCGGGNAGGAA 240
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      396 CCCFTCTCCGACAGATGCCAGGCTCCAGCTGATTAAGACTGATTTCTCGGAAAGGAA 455

Qy      241 ATGAAGTGTGATTTTGTCTCAGACTTTACATATGAAGTTTCACACCTGGCTCCGCCCAAT 300
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      456 ATGAAGTTATATTTTGTCTCAGACCTTACATATGAAGCTCACACCTGGCTCCGCCAAT 515

Qy      301 CCGGACAAACAGTTCCTCATCTCCCTCGCGGCTCTCTCTCCGTTGGCTGGAACAAGTA 360
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      516 CCAGACAAGCAGTTTCTGATCTCCCTCTCCGCCCTCTCCGCCAGTGGGATGAAACAAGTG 575

Qy      361 GAAGATGCCACCCCGCTCATAAATTAGCATCTTTTATATGTCATCTCTCCAAGCTGGGGCCA 420

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DB	576	GAAGATGGACCCGAGTCATAAACTATGATCTCTTATATGCCATCTCTCAAGCTTGGGGCCA	635
QY	421	GGAGAGAAGTATGAACTGCATGCAGCGACACACCCACTCCCTCAGTGTGGTGGTCCACGTG	480
DB	636	GGGAAAAGTATGAATTGCACCGACGCACTGACACCACTCCACGCTGGTGGTCAATGTA	695
QY	481	TGTGAGAGTGCACCAAGAGAATGAGGAGGAAGGAAGAGATGAGAGAATGAAGAGACCC	540
DB	696	TGTGAGAGTGATCAAGAGAAGGAGGAGGAAGAGGAA---ATGGAAAGAANTCAGGAGACCT	752
QY	541	AAGCCCCAAAATCATCCAGACACGGAGACCGGAGTACACACCGATCCACCTTTAGCTGA	597


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QY 121 AAGGACACACCTTCCAGTATTTTAAAGCTTTCAAAACGTTCCGGGATAAACTTTCAGCAAC 180
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Db 157 AAGGACACACCTTTCAGTATTTTAAAGCTTTCAAAACGTTCCGGGATAAACTTTCAGCAAC 216
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 CCCTTATCTGCAGCGAGTCCAGGCTGGCGTGCACAGACCGAGTTCCTGGGGAAGGAA 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 217 CCCTTCTCCGACGAGATGCCAGGCTCCAGCTGCATAGACACTGAGTTCTGGGAAGGAA 276
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QY 241 ATGAAGTTGTTATTTTGGCTCAGACTTTACACATAGGAAGTTTACACCTGCTCCGCCCAAT 300
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Db 277 ATGAAGTTATATTTTGGCTCAGACTTTACACATAGGAAGTTTACACCTGCTCCGCCCAAT 336
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QY 301 CCGCAACAACAGTTCCTCATCTCCCTCCGGGCTCTCTCCGTTGGTGGGAAACAAGTA 360
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QY 361 GAAGATGCCACCCCGTCTATAATACGATCTTTATATATGCTTCCAGCTGGGGCCA 420
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Db 397 GAAGATGGGACCCCGTCTATAATACGATCTTTATATATGCTTCCAGCTGGGGCCA 456
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QY 421 GGAGAGAAGTATGAAGTGCATGACGACGACAGACCCACTCCAGTGTGGTGTCCACGTG 480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 457 GG-GAAAGTATGATGACGACGAGGACTGACACCACTCCAGCGTGTGGTCCATGTA 515
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QY 481 TGTGAGATGACCAAGAGAAATGAGGAGGAGGAGAGATGGAGAGAAATGAAGAGACCC 540
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Db 516 TGTGAGATGATCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 572
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QY 541 AAGCCCAAAATCATCCAGACACGAGACGGAGTACACACCGATCCACCTTACGTGA 597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 573 AAGCCCAAAATTTATCCAGACGAGGAGGAGGAGGAGTACACCGATCCACCTCAGCTGA 629
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RESULT 9
LOCUS BQ427531
DEFINITION AGENCOURT_7914139 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6156873
5', mRNA sequence.
ACCESSION BQ427531
VERSION BQ427531.1 GI:21166607
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 867)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Cloning Distribution: Agencourt Bioscience Corporation
Cloning Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL3501 row: n column: 10
High quality sequence stop: 626.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Site:2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
204 a 241 c 267 g 155 t

BASE COUNT
ORIGIN

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Query Match 78.6%; Score 469.2; DB 14; Length 867;
Best Local Similarity 88.8%; Pred. No. 1.7e-114;
Matches 531; Conservative 0; Mismatches 63; Indels 4; Gaps 2;

QY 1 ATGGAGGAGGTGATGTCGAGGACCTGCGGAGGCGCCACCATGCGCTGCCACCTGGAGCCCG 60
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QY 61 CCGCTGTTCTGGAGCGCTGTGCGGGCCAAATTTGAATCCCTCTTCAGAACATATGAC 120
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Db 215 CCGCTGTTCTGGAGCGCTGTGCGGGCCAAATTTGAATCCCTCTTCAGAACATATGAC 274
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QY 121 AAGGACACACCTTCCAGTATTTTAAAGCTTTCAAAACGTTCCGGGATAAACTTTCAGCAAC 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 275 AAGGACACACCTTTCAGTATTTTAAAGCTTTCAAAACGTTCCGGGATAAACTTTCAGCAAC 334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 CCGTTATCTGCAGCGATGCCAGGCTGCGGCTGCACAAGACCGAGTTCCTGGGGAAGGAA 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 335 CCGTTCTCCGACGAGATGCCAGGCTCCAGCTGCATAGACACTGAGTTCTGGGGAAGGAA 394
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QY 241 ATGAAGTTTATTTTCTGCTCAGACTTTACACATAGGAAGTTTCAACCTGCTCCGCCCAAT 300
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Db 395 ATGAAGTTTATTTTCTGCTCAGACTTTACACATAGGAAGTTTCAACCTGCTCCGCCCAAT 454
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QY 301 CCGCAACAACAGTTCCTCATCTCCCTCCGGGCTCTCTCCGTTGGTGGGAAACAAGTA 360
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Db 455 CCAGACAAGAGTTCCTGATCTCCCTCCGGCTCTCCGCAAGTGGGATGGAAACAAGTG 514
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 GAAGATGCCACCCCGTCTATAATACGATCTTTATATGCTTCCAGCTGGGGCCA 420
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Db 515 GAAGATGCCACCCCGTCTATAATACGATCTTTATATGCTTCCAGCTGGGGCCA 574
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QY 421 GGAGAGAAGTATGAAGTGCATGACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
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QY 481 TGTGAGAGTGAACCAAGAGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
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Db 635 TGTGAGAGTGAACCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 691
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QY 541 AAGCCCAAAATCATCCAGACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 597
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Db 692 AAGCCCAAAATTTATCCAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 749
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RESULT 10
LOCUS AL551657
DEFINITION AL551657 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1063YH22 5
prime, mRNA sequence.
ACCESSION AL551657
VERSION AL551657.1 GI:12889816
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 923)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1..923
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/db_xref="taxon:9606"
/clone="CS0D1063YH22"
/clone_lib="LTI_NFL006.PL2"
/tissue_type="placenta"

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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cnapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10891 row: n column: 03
High quality sequence stop: 711.

Location/Qualifiers
1. 711
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/clone_lib="NCI_CGAP_Mam4"
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/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI; Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."

196 a 184 c 183 g 148 t

BASE COUNT
ORIGIN

Query Match 78.0%; Score 465.4; DB 13; Length 711;
Best Local Similarity 98.4%; Pred. No. 1.6e-113;
Matches 491; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

Qy 84 CCGGGCAAAATTTGAATCCCTCTTCAGAACATATGACAGGACACCCCTTCAGTATTT 143

Db 62 CCAGGGCAAAATTTGAATCCCTCTTCAGAACATATGACAGGACACCCCTTCAGTATTT 121

Qy 144 TAAGAGCTTCAAAAGTGTCCGGATAAACTTCAGCAACCCCTTATCTGCGCCGATGCCAG 203

Db 122 TAAGAGCTTCAAAAGTGTCCGGATAAACTTCAGCAACCCCTTATCTGCGCCGATGCCAG 181

Qy 204 GCTGCGCTGCACAGACCGAGTTCCTGGGGAAGGAAATGAAGTTGTATTTTCTCAGAC 263

Db 182 GCTGCGCTGCACAGACCGAGTTCCTGGGGAAGGAAATGAAGTTGTATTTTCTCAGAC 241

Qy 264 TTTACATAGGAAGTTTCACACCTGGCTCGGCCCAATCCCGACAAACAGTTCTCTCATCTC 323

Db 242 TTTACATAGGAAGTTTCACACCTGGCTCGGCCCAATCCCGACAAACAGTTCTCTCATCTC 301

Qy 324 CCCTCCGGCCCTCT-CCTCCGCTGGTGGAAACAGTAGAAGATGCCACCCCGTCTATAA 382

Db 302 CCCTCGGCCCTCTCCCTCCGCTGGGCTGGAAACAAGTAGAAGATGCCACCCCGTCTATAA 361

Qy 383 ATTACGATCTTTTATATGCCATCTCCAAAGTGGGCCAGGAGAGAAGTATGAATGCGATG 442

Db 362 ATTACGATCTTTTATATGCCATCTCCAAAGTGGGCCAGGAGAGAAGTATGAATGCGATG 421

Qy 443 CAGCGACAGACCCCACTCCCAAGTGTGGTGTCCAGTGTGTGAGAGTGCACCAAGAGATG 502

Db 422 CAGCGACAGACCCCACTCCCAAGTGTGGTGTCCAGTGTGTGAGAGTGCACCAAGAGATG 481

Qy 503 AGGAGGAAGAGAGAGATGAGAGAGATGAGAGACCCAGCCCAAAATCATCTCAGACAC 562

Db 482 AGGAGGAAGAGAGAGATGAGAGAGATGAGAGACCCAGCCCAAAATCATCTCAGACAC 540

Qy 563 GGAGACCGGAGTACACACC 581

Db 541 GGAGACCGGAGTACACACC 559

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cnapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10891 row: n column: 03
High quality sequence stop: 711.

Location/Qualifiers
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/clone_image="IMAGE:4945346"
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/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI; Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."

210 a 257 c 295 g 155 t

BASE COUNT
ORIGIN

Query Match 78.5%; Score 468.6; DB 9; Length 923;
Best Local Similarity 88.4%; Pred. No. 2.5e-114;
Matches 528; Conservative 3; Mismatches 62; Indels 4; Gaps 2;

Qy 1 ATGGAGGAGGTGGATCTGCAGGACCTGCCGAGGCCACCATCGCTGCCACCTGGACCCG 60

Db 257 ATGGAGGAGGTGGATCTGCAGGACCTGCCGAGGCCACCATCGCTGCCACCTGGACCCG 316

Qy 61 CGCTGTTCGCGGACGCGCTGTCCGGGCCAAATTTGAATCCCTCTTCAGAACATATGAC 120

Db 317 CGCTGTTCGCGGACGCGCTGTCCGGGCCAAATTTGAATCCCTCTTCAGAACATATGAC 376

Qy 121 AAGGACACACCTCCAGTATTTAAGAGCTTCAAGCTGTCCGATAAACTTCAGCAAC 180

Db 377 AAGGACATCACCTTCAGTATTTAAGAGCTTCAAGCTGTCCGATAAACTTCAGCAAC 436

Qy 181 CCCTTATCTGACGCGATGCCAGGCTCGGCTGCACAGACCGAGTTCCTGGGGAAGAA 240

Db 437 CCCTTCTCGGACGAGATGCCAGGCTCCAGCTGCATTAARACTGAGTTCTGGGAAGAA 496

Qy 241 ATGAAGTTGTATTTGCTCAGACTTTACATAGAGTTTACACCTGGCTCCGCCCAAT 300

Db 497 ATGAAGTTGTATTTGCTCAGACTTTACATAGAGTTTACACCTGGCTCCGCCCAAT 556

Qy 301 CCGCAACACAGTCTCTCATCTCCCTCCGCGCTCTCTCCGCTGGTGGGAAACAAGTA 360

Db 557 CAGAGACAGATTTCTGATCTCCCTCCGCGCTCTCCGCGCTGGGATGGAACAAGTG 616

Qy 361 GAAGATGCCACCCCGCTCAATAATTCAGATCTTTTATATGCGATCTCAACCTGGGGCA 420

Db 617 GAAGATGCCACCCCGCTCAATAATTCAGATCTTTTATATGCGATCTCAACCTGGGGCA 676

Qy 421 GGAGAGATGTAAGTGTATGATCGAGACAGACCCCTCCAGTGTGGTGTCCACCTG 480

Db 677 GGGGAAAGTATGAATTCAGCAGCGGACTGACACCTCCAGCGTGGTGTCCATGTA 736

Qy 481 TGTGAGAGTGACCAAGAGATGAGGAGGAAGAGAGATGGAGAGATGAGAGACCC 540

Db 737 TGTGAGAGTGATCAAGAGAGGAGGAAGAGAGAA--ATGGAAGAATGAGGAGA-CT 792

Qy 541 AAGCCCAAAATATCCAGACAGGAGACCGGAGTAGTACACACCATCCACTTACCTGA 597

Db 793 AAGCCCAAAATATCCAGACAGGAGGCGGAGTAGTACACCGCATCCACTCAGCTGA 849

RESULT 11
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LOCUS 602815815F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4945346 5', mRNA sequence.
DEFINITION

ACCESSION BG915568.1 GI:14296044
VERSION BG915568
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 711)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)


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RESULT 12
BF782633
LOCUS
DEFINITION
602107462F1 NCL_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4236038
5', mRNA sequence.
ACCESSION
BF782633
VERSION
BF782633.1 GI:12087669
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 950)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9843 row: k column: 15
High quality sequence stop: 701.
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/db_xref="taxon:10090"
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/clone_lib="NCL_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: Kidney; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCL_CGAP Library. |"
BASE COUNT 220 a 257 c 274 g 199 t
ORIGIN
source
Query Match 77.6%; Score 463.4; DB 12; Length 950;
Best Local Similarity 96.3%; Pred. No. 6.2e-113;
Matches 517; Conservative 0; Mismatches 16; Indels 4; Gaps 4;
QY 64 GTCTTCGTGACGCGCTGTGCGGGCCAAATTTGAATCCCTCTTCAGACATATGACAAG 123
Db 138 GTCTTCGCGAAGTGAGACGACGAGCCAAATTTGAATCCCTCTTCAGACATATGACAAG 197
QY 124 GACACACCTTCCAGTATTTTAAGAGCTTCAAACGTTCCGCGATATAAATTCAGCAACCCC 183
Db 198 GACACACCTTCCAGTATTTTAAGAGCTTCAAACGTTCCGCGATATAAATTCAGCAACCCC 257
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Db 258 TTATCTGACGCGATGCGAGCTGCGGTGTCACAAGACCGAGTTCCTGGGGAAGGAATG 317
QY 244 AAGTTCTATTTTCTCAGACTTTACACATAGGAAGTTCAACCTGCTCGGCCCAATCCC 303
Db 318 AAGTTCTATTTTCTCAGACTTTACACATAGGAAGTTCAACCTGCTCGGCCCAATCCC 376
QY 304 GACAAACAGTTCTCATCTCCCTCCGGCTCTCCCTCCCTGCTGGCTGGAAACAAGTAGAA 363
Db 377 GACAAACAGTTCTCATCTCCCTCCGGCTCTCCCTCCCTGCTGGCTGGAAACAAGTAGAA 436
QY 364 GATGCCACCCCGTCATAAATTACGATCTTTTATATGCCATCTCCAGCTGGGGCCAGGA 423
Db 437 GATGCCACCCCGTCATAAATTACGATCTTTTATATGCCATCTCCAGCTGGGGCCAGGA 496
QY 424 GAGAAATGTAAGTGTGATGATGAGCGAGACACCCCACTCCCAAGT-GTGGTGTCCACGTGTG 482
Db 497 GAGAAATGTAAGTGTGATGATGAGCGAGACACCACTCCCAAGTGTGGTGTGTCCACGTGTG 556
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QY 483 TGAGAGTGACCAAGAGAATGAGGAGGAAGAGAA-GAGATGGAGAGAATG-AAAGAGACCC 540
Db 557 TGAGAGTGACCAAGAGAATGAGGAGGAAGAGAAAGAGATGGAGAGAATGAAAGAGACCC 616
QY 541 AAGCCCAAAATATCCAGACACGAGACCGGAGTACACACCGATCCACCTTAGCTGA 597
Db 617 AAGCCCAAAATATCCAGACACGAGACCGGAGTACACACCGATCCCAACTCAGCTGA 673
RESULT 13
BG296537
LOCUS
DEFINITION
602394441F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4506130 5',
mRNA sequence.
ACCESSION
BG296537
VERSION
BG296537.1 GI:13059271
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 980)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10381 row: a column: 11
High quality sequence start: 3
High quality sequence stop: 747.
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/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 265 a 258 c 269 g 188 t
ORIGIN
source
Query Match 77.3%; Score 461.4; DB 12; Length 980;
Best Local Similarity 96.2%; Pred. No. 2.2e-112;
Matches 505; Conservative 0; Mismatches 16; Indels 4; Gaps 3;
QY 64 GTCTTCGTGACGCGCTGTGCGGGCCAAATTTGAATCCCTCTTCAGACATATGACAAG 123
Db 148 GTCTTCAGCGAAAGTAGATGATGAGAGCTTCAAACGTTCCGCGATATAAATTCAGCAACCCC 207
QY 124 GACACACCTTCCAGTATTTTAAGAGCTTCAAACGTTCCGCGATATAAATTCAGCAACCCC 183
Db 208 GACACACCTTCCAGTATTTTAAGAGCTTCAAACGTTCCGCGATATAAATTCAGCAACCCC 267
QY 184 TTATCTGACGCGATGCGAGCTGCGGTGTCACAAGACCGAGTTCCTGGGGAAGGAATG 243
Db 268 TTATCTGACGCGATGCGAGCTGCGGTGTCACAAGACCGAGTTCCTGGGGAAGGAATG 327
QY 244 AAGTTGTATTTTCTCAGACTTTACACATAGGAAGTTCAACCTGCTCGGCCCAATCCC 303
Db 328 AAGTTGTATTTTCTCAGACTTTACACATAGGAAGTTCAACCTGCTCGGCCCAATCCC 386
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